

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 13, 2006, 06:41:04 ; Search time 73 Seconds
(without alignments)
335.233 Million cell updates/sec

Title: US-10-601-311-1_COPY_143_438
Perfect score: 1563
Sequence: 1 KTMNDFYKLLGKGTGKV.....VPPFKQVTSYDTRFYDDEE 296

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pap:*
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3: /cgn2_6/ptodata/1/1aa/H COMB.pap:*
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5: /cgn2_6/ptodata/1/1aa/RE COMB.pap:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563	100.0	465	2	US-09-526-043-2
2	1563	100.0	479	2	US-09-771-161A-246
3	1563	100.0	479	2	US-09-771-161A-247
4	1563	100.0	479	2	US-09-771-161A-248
5	1558	99.7	454	2	US-09-526-043-17
6	1394.5	89.2	480	2	US-09-590-740-6
7	1393.5	89.2	480	2	US-09-091-058-2
8	1393.5	89.2	480	2	US-09-590-740-2
9	1393.5	89.2	480	2	US-09-538-092-1053
10	1393.5	89.2	480	2	US-09-526-043-14
11	1393.5	89.2	480	2	US-09-771-161A-223
12	1393.5	89.2	726	2	US-09-417-197-71
13	1393.5	89.2	727	2	US-09-417-197-139
14	1391	89.0	480	2	US-09-526-043-13
15	1391	89.0	481	2	US-09-538-092-1054
16	1368.5	87.6	480	2	US-09-205-658-157
17	1364	87.3	417	2	US-09-590-740-4
18	1118.5	71.6	546	2	US-09-205-658-155
19	1107	70.8	352	2	US-09-771-161A-157
20	1098	70.2	541	2	US-09-205-658-154
21	1037	65.7	483	2	US-09-205-658-156
22	856	54.8	407	2	US-10-067-977-4
23	856	54.8	445	2	US-10-067-977-2
24	852	54.5	431	2	US-09-031-295-2
25	852	54.5	431	2	US-10-000-038-2
26	851.5	54.5	430	1	US-08-712-709-9
27	851.5	54.5	430	2	US-09-111-444-9

28	851.5	54.5	430	2	US-09-541-228-9	Sequence 9, Appli
29	848	54.3	431	1	US-08-712-709-5	Sequence 5, Appli
30	848	54.3	431	2	US-09-111-444-5	Sequence 5, Appli
31	848	54.3	431	2	US-09-541-228-5	Sequence 4, Appli
32	819.5	52.4	737	2	US-09-772-647-4	Sequence 4, Appli
33	819.5	52.4	737	2	US-10-228-931-4	Sequence 4, Appli
34	819.5	52.4	737	2	US-09-771-161A-195	Sequence 195, Appli
35	815	52.1	682	2	US-09-538-092-1003	Sequence 1003, Ap
36	815	52.1	739	2	US-09-949-016-7606	Sequence 7606, Ap
37	799.5	51.2	604	2	US-09-949-016-7547	Sequence 7547, Ap
38	790	50.5	671	6	5266464-2	Patent No. 5266464
39	779	49.8	673	2	US-09-538-092-853	Sequence 853, App
40	777	49.7	672	2	US-10-092-138A-27	Sequence 27, Appl
41	777	49.7	672	2	US-09-538-092-943	Sequence 943, Appl
42	777	49.7	672	2	US-08-681-219A-27	Sequence 27, Appl
43	771	49.3	916	2	US-09-417-197-73	Sequence 73, Appl
44	768.5	49.2	587	1	US-08-313-274-2	Sequence 2, Appli
45	768.5	49.2	655	2	US-09-949-016-11676	Sequence 11676, A

ALIGNMENTS

RESULT 1
US-09-526-043-2
; Sequence 2, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526, 043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-526-043-2

Query Match	100.0%	Score 1563;	DB 2;	Length 465;
Best Local Similarity	100.0%	Pred. No. 8.4e-141;	Mismatches 0;	Indels 0; Gaps 0;
Matches 296;	Conservative	0;		
Qy	1	KTMNDFYKLLGKGTGKVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN	60	
Db	143	KTMNDFYKLLGKGTGKVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN	202	
Qy	61	TRHPFLTSIKYSFQKRLCFVMEYVNGGELFFHLSRVRVSESDTRFYGABIVSALDYL	120	
Db	203	TRHPFLTSIKYSFQKRLCFVMEYVNGGELFFHLSRVRVSESDTRFYGABIVSALDYL	262	
Qy	121	HSGKIVYRDLKLENLMKDGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND	180	
Db	263	HSGKIVYRDLKLENLMKDGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND	322	
Qy	181	YGRAVDWNGLVVYEMWCGRLPFYVQDHEKLFELIMEDIKFPRTLSDAKSLLSGLLI	240	
Db	323	YGRAVDWNGLVVYEMWCGRLPFYVQDHEKLFELIMEDIKFPRTLSDAKSLLSGLLI	382	
Qy	241	KDPNKRLLGGGDDAKKIMRHSFFSGVNVQDYYDKLVPPFKPQVTSYDTRFYDDEE	296	
Db	383	KDPNKRLLGGGDDAKKIMRHSFFSGVNVQDYYDKLVPPFKPQVTSYDTRFYDDEE	438	

RESULT 2
US-09-771-161A-246

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; Sequence 246, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-246

Query Match      100.0%; Score 1563; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.8e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 240
Db 323 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 3
US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-247

Query Match      100.0%; Score 1563; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.8e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 240
Db 323 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 4
US-09-771-161A-248
; Sequence 248, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 248
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match      100.0%; Score 1563; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.8e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 240
Db 323 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 5
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

Query Match      100.0%; Score 1563; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.8e-141;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDFFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 240
Db 323 YGRAVDWVGLGVVYEMVCMGRLPFYNQDHEKLFELIIMEDIKFPRTLTSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438
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US-09-526-043-17
; Sequence 17, Application US/09526043
; Patent No. 6681555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-526-043-17

Query Match 99.7%; Score 1558; DB 2; Length 454;
Best Local Similarity 99.7%; Pred. No. 2.5e-140;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGYKAMKILKEVIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGYKAMKILKEVIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDLKLENLMDKGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 263 HSGKIVYRDLKLENLMDKGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 322

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 382

QY 241 KDPNKRLLGGGPPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

RESULT 6
US-09-590-740-6
; Sequence 6, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-590-740-6

Query Match 89.2%; Score 1394.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.1e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TMDNFDYLLKLGKGTGKVIIVREKASGYKAMKILKEVIAKDEVAHTLTESRVLKN 61
DB 146 TMDNFDYLLKLGKGTGKVIIVREKATGRYVAMKILKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 121
DB 206 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 265

QY 122 SGK-IVYRDLKLENLMDKGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 266 SGKVVYRDLKLENLMDKGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 385

QY 241 KDPNKRLLGGGPPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 386 KDPNKRLLGGGPPDDAKEIMRHSFFAGIVQHVVYKILSPFPKQVTSSETDTRYFDEE 441

RESULT 8
US-09-590-740-2
; Sequence 2, Application US/09590740
; Patent No. 6689807

QY 2 TMDNFDYLLKLGKGTGKVIIVREKASGYKAMKILKEVIAKDEVAHTLTESRVLKN 61
DB 146 TMDNFDYLLKLGKGTGKVIIVREKATGRYVAMKILKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 121
DB 206 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 265

QY 122 SGK-IVYRDLKLENLMDKGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 266 SGKVVYRDLKLENLMDKGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 385

QY 241 KDPNKRLLGGGPPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 386 KDPNKRLLGGGPPDDAKEIMRHSFFAGIVQHVVYKILSPFPKQVTSSETDTRYFDEE 441

RESULT 7
US-09-091-058-2
; Sequence 2, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Matthias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091,058
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-091-058-2

Query Match 89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TMDNFDYLLKLGKGTGKVIIVREKASGYKAMKILKEVIAKDEVAHTLTESRVLKN 61
DB 146 TMDNFDYLLKLGKGTGKVIIVREKATGRYVAMKILKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 121
DB 206 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 265

QY 122 SGK-IVYRDLKLENLMDKGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 266 SGKVVYRDLKLENLMDKGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 385

QY 241 KDPNKRLLGGGPPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 386 KDPNKRLLGGGPPDDAKEIMRHSFFAGIVQHVVYKILSPFPKQVTSSETDTRYFDEE 441

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; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-740-2

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
Db  146  TMNEFEYLKLGKGTGKVLVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy  62  RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRERVSFSEDRTRFYGAEIVSALDYHL 121
Db  206  RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSSRERVSFSEDRARFYGAEIVSALDYHL 265

Qy  122  SGK-IVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db  266  SEKNVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEVLEDND 325

Qy  181  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db  326  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEERFRTLGPPEAKSLLSGLLK 385

Qy  241  KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPPKPQVTSSTDTRYFDEE 296
Db  386  KDPKQRLGGGSEDAKEIMQHRFFAGIVMHHVYKKSPPPKPQVTSSTDTRYFDEE 441

RESULT 9
US-09-538-092-1053
; Sequence 1053, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Ioic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1053
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P31749
US-09-538-092-1053

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
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; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-740-2

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
Db  146  TMNEFEYLKLGKGTGKVLVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy  62  RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRERVSFSEDRTRFYGAEIVSALDYHL 121
Db  206  RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSSRERVSFSEDRARFYGAEIVSALDYHL 265

Qy  122  SGK-IVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db  266  SEKNVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEVLEDND 325

Qy  181  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db  326  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEERFRTLGPPEAKSLLSGLLK 385

Qy  241  KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPPKPQVTSSTDTRYFDEE 296
Db  386  KDPKQRLGGGSEDAKEIMQHRFFAGIVMHHVYKKSPPPKPQVTSSTDTRYFDEE 441

RESULT 10
US-09-526-043-14
; Sequence 14, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-526-043-14

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
Db  146  TMNEFEYLKLGKGTGKVLVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy  62  RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRERVSFSEDRTRFYGAEIVSALDYHL 121
Db  206  RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSSRERVSFSEDRARFYGAEIVSALDYHL 265

Qy  122  SGK-IVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db  266  SEKNVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEVLEDND 325

Qy  181  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db  326  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEERFRTLGPPEAKSLLSGLLK 385

Qy  241  KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPPKPQVTSSTDTRYFDEE 296
Db  386  KDPKQRLGGGSEDAKEIMQHRFFAGIVMHHVYKKSPPPKPQVTSSTDTRYFDEE 441

RESULT 11
US-09-771-161A-223
; Sequence 223, Application US/09771161A
; Patent No. 6938450
; GENERAL INFORMATION:
```


APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 223
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-223

Query Match 89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TWNDFYKLSYFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 61
DB 146 TWNEFEYKLLGKGTGFKVILVREKATGRYAMKILKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSDDRARFYGAIEVSALDYH 265

QY 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 266 SEKVVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEEIRFPRTLGPPEAKSLGLLK 385

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSDDTRYFDEE 296
DB 386 KDPKORLGGSGEDAKEIMQHRRFFAGIVWQHVYEKLSPPFKPQVTSDDTRYFDEE 441

RESULT 12
US-09-417-197-71
; Sequence 71, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
US-09-417-197-71

Query Match 89.2%; Score 1393.5; DB 2; Length 726;
Best Local Similarity 87.8%; Pred. No. 2.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TWNDFYKLSYFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 61
DB 146 TWNEFEYKLLGKGTGFKVILVREKATGRYAMKILKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSDDRARFYGAIEVSALDYH 265

QY 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 266 SEKVVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEEIRFPRTLGPPEAKSLGLLK 385

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSDDTRYFDEE 296
DB 386 KDPKORLGGSGEDAKEIMQHRRFFAGIVWQHVYEKLSPPFKPQVTSDDTRYFDEE 441

RESULT 13
US-09-417-197-139
; Sequence 139, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PKB fusion
US-09-417-197-139

Query Match 89.2%; Score 1393.5; DB 2; Length 727;
Best Local Similarity 87.8%; Pred. No. 2.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TWNDFYKLSYFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 61
DB 393 TWNEFEYKLLGKGTGFKVILVREKATGRYAMKILKEVIAKDEVAHTLTENRVLQNS 452

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 121
DB 453 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSDDRARFYGAIEVSALDYH 512

QY 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 513 SEKVVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 572

QY 181 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 573 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEEIRFPRTLGPPEAKSLGLLK 632

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSDDTRYFDEE 296
DB 633 KDPKORLGGSGEDAKEIMQHRRFFAGIVWQHVYEKLSPPFKPQVTSDDTRYFDEE 688

RESULT 14
US-09-526-043-13
; Sequence 13, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF

APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 223
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-223

Query Match 89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TWNDFYKLSYFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 61
DB 146 TWNEFEYKLLGKGTGFKVILVREKATGRYAMKILKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSDDRARFYGAIEVSALDYH 265

QY 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 266 SEKVVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEEIRFPRTLGPPEAKSLGLLK 385

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSDDTRYFDEE 296
DB 386 KDPKORLGGSGEDAKEIMQHRRFFAGIVWQHVYEKLSPPFKPQVTSDDTRYFDEE 441

RESULT 12
US-09-417-197-71
; Sequence 71, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
US-09-417-197-71

Query Match 89.2%; Score 1393.5; DB 2; Length 726;
Best Local Similarity 87.8%; Pred. No. 2.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TWNDFYKLSYFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 61
DB 146 TWNEFEYKLLGKGTGFKVILVREKATGRYAMKILKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSDDRARFYGAIEVSALDYH 265

QY 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 266 SEKVVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEEIRFPRTLGPPEAKSLGLLK 385

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSDDTRYFDEE 296
DB 386 KDPKORLGGSGEDAKEIMQHRRFFAGIVWQHVYEKLSPPFKPQVTSDDTRYFDEE 441

RESULT 13
US-09-417-197-139
; Sequence 139, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139
; LENGTH: 727
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
US-09-417-197-139

Query Match 89.2%; Score 1393.5; DB 2; Length 727;
Best Local Similarity 87.8%; Pred. No. 2.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TWNDFYKLSYFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 61
DB 393 TWNEFEYKLLGKGTGFKVILVREKATGRYAMKILKEVIAKDEVAHTLTENRVLQNS 452

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSDDRTRFYGAIEVSALDYH 121
DB 453 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSDDRARFYGAIEVSALDYH 512

QY 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180
DB 513 SEKVVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 572

QY 181 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 573 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEEIRFPRTLGPPEAKSLGLLK 632

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSDDTRYFDEE 296
DB 633 KDPKORLGGSGEDAKEIMQHRRFFAGIVWQHVYEKLSPPFKPQVTSDDTRYFDEE 688

RESULT 14
US-09-526-043-13
; Sequence 13, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF

```
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526.043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125.108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 13
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
;
Query Match      89.0%; Score 1391; DB 2; Length 480;
Best Local Similarity 86.4%; Pred. No. 2.3e-124;
Matches 255; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

Qy  2  TMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKNT 61
Db 148 TMNDFYLLKLGKGTGKVIIVREKATGRYYAMKILRAKEVIAKDEVAHTVTSRVLQNT 207

Qy  62  RHPFLTSIKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYIH 121
Db 208 RHPFLTALKYAFQTHDRLCFVMEYANGGELFFHLSRERVTEERARFYGAIVSALEYLH 267

Qy 122 SGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLENDY 181
Db 268 SRDVVYRDLEKLENMLDKDGHIKITDFGLCKEGISDGTATMKTFCGTPEYLAPEVLENDY 327

Qy 182 GRAVDWMLGLGVVMYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLSLGLLIK 241
Db 328 GRAVDWMLGLGVVMYEMMCGRLPFYVNDQHEKLFELILMEEIRFPRTLSPKSLLAGLLKK 387

Qy 242 DPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSETDTRYFDEE 296
Db 388 DPKQRLGGGSDAKEVMEHRRFLLSINWQDVVQKKLLPPFKPQVTSEVDTRYFDDDE 442
```

```
RESULT 15
; Sequence 1054, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538.092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1054
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P31751
;
US-09-538-092-1054
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Query Match      89.0%; Score 1391; DB 2; Length 481;
Best Local Similarity 86.4%; Pred. No. 2.3e-124;
Matches 255; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

Qy  2  TMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKNT 61
Db 148 TMNDFYLLKLGKGTGKVIIVREKATGRYYAMKILRAKEVIAKDEVAHTVTSRVLQNT 207
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Qy  62  RHPFLTSIKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYIH 121
Db 208 RHPFLTALKYAFQTHDRLCFVMEYANGGELFFHLSRERVTEERARFYGAIVSALEYLH 267

Qy 122 SGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLENDY 181
Db 268 SRDVVYRDLEKLENMLDKDGHIKITDFGLCKEGISDGTATMKTFCGTPEYLAPEVLENDY 327

Qy 182 GRAVDWMLGLGVVMYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLSLGLLIK 241
Db 328 GRAVDWMLGLGVVMYEMMCGRLPFYVNDQHEKLFELILMEEIRFPRTLSPKSLLAGLLKK 387

Qy 242 DPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSETDTRYFDEE 296
Db 388 DPKQRLGGGSDAKEVMEHRRFLLSINWQDVVQKKLLPPFKPQVTSEVDTRYFDDDE 442
```

Search completed: February 13, 2006, 06:43:19
Job time : 74 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 13, 2006, 06:59:09 ; Search time 281 Seconds
(without alignments)
440.133 Million cell updates/sec

Title: US-10-601-311-1_COPY_143_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFGKV.....VPPFKPQVTSRTDTRYFDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563	100.0	465	3	US-09-526-043-2
2	1563	100.0	465	4	US-10-394-568-2
3	1563	100.0	465	4	US-10-394-568-12
4	1563	100.0	465	6	US-11-063-691-2
5	1563	100.0	479	3	US-09-771-161A-246
6	1563	100.0	479	3	US-09-771-161A-247
7	1563	100.0	479	3	US-09-771-161A-248
8	1563	100.0	479	4	US-10-394-322A-3
9	1563	100.0	479	4	US-10-217-574-33
10	1563	100.0	479	4	US-10-217-555-33
11	1563	100.0	479	5	US-10-753-267-108
12	1558	99.7	454	3	US-09-526-043-17
13	1558	99.7	454	6	US-11-063-691-17
14	1394.5	89.2	320	4	US-10-116-722A-5
15	1394.5	89.2	480	4	US-10-713-678-6
16	1394.5	89.2	501	5	US-10-732-923-10650
17	1394.5	89.2	763	5	US-10-732-923-10649
18	1393.5	89.2	320	4	US-10-116-722A-7
19	1393.5	89.2	480	3	US-09-771-161A-223
20	1393.5	89.2	480	3	US-09-970-000-4
21	1393.5	89.2	480	3	US-09-526-043-14
22	1393.5	89.2	480	4	US-10-060-065-18
23	1393.5	89.2	480	4	US-10-059-585-39
24	1393.5	89.2	480	4	US-10-394-322A-1
25	1393.5	89.2	480	4	US-10-217-574-31
26	1393.5	89.2	480	4	US-10-217-555-31
27	1393.5	89.2	480	4	US-10-701-490-4

28	1393.5	89.2	480	4	US-10-713-678-2	Sequence 2, Appli
29	1393.5	89.2	480	4	US-10-746-545-36	Sequence 16, Appli
30	1393.5	89.2	480	5	US-10-735-118-1	Sequence 1, Appli
31	1393.5	89.2	480	5	US-10-621-485A-1	Sequence 1, Appli
32	1393.5	89.2	480	5	US-10-823-433-4	Sequence 4, Appli
33	1393.5	89.2	480	6	US-11-063-691-14	Sequence 14, Appli
34	1393.5	89.2	492	3	US-09-955-999-96	Sequence 96, Appli
35	1393.5	89.2	524	4	US-10-103-256-11	Sequence 11, Appli
36	1393.5	89.2	524	4	US-10-365-348-11	Sequence 11, Appli
37	1393.5	89.2	726	4	US-10-072-036-71	Sequence 71, Appli
38	1393.5	89.2	727	4	US-10-072-036-139	Sequence 139, Appli
39	1391	89.0	315	4	US-10-746-545-22	Sequence 22, Appli
40	1391	89.0	315	4	US-10-746-545-23	Sequence 23, Appli
41	1391	89.0	315	6	US-11-021-951-163	Sequence 163, Appli
42	1391	89.0	319	4	US-10-116-722A-6	Sequence 6, Appli
43	1391	89.0	319	4	US-10-116-722A-8	Sequence 8, Appli
44	1391	89.0	335	4	US-10-746-545-24	Sequence 24, Appli
45	1391	89.0	335	4	US-10-746-545-37	Sequence 37, Appli

ALIGNMENTS

RESULT 1

US-09-526-043-2

; Sequence 2, Application US/09526043

; Publication No. US20030100049A1

; GENERAL INFORMATION:

; APPLICANT: Guo, Kun

; APPLICANT: Pagnoni, Marco

; APPLICANT: Clark, Kenneth

; APPLICANT: Ivashchenko, Yuri

; TITLE OF INVENTION: ART NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF

; FILE REFERENCE: A3278A-US

; CURRENT APPLICATION NUMBER: US/09/526.043

; EARLIER FILING DATE: 2000-03-14

; EARLIER APPLICATION NUMBER: 60/125,108

; EARLIER FILING DATE: 1999-03-19

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 465

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-526-043-2

Query Match 100.0%; Score 1563; DB 3; Length 465;

Best Local Similarity 100.0%; Pred. No. 2.1e-111;

Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKTFGKVILVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60

Db 143 KTMNDFYLLKLGKTFGKVILVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLSLKYSFQTKORLCFVMEYVNGGELFPHLSRERFSEDRTRFYGAIVSALDYL 120

Db 203 TRHPFLSLKYSFQTKORLCFVMEYVNGGELFPHLSRERFSEDRTRFYGAIVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKOGHKITDPLGCKEGITDAATWKTFCGTPPYLAPEVLEND 180

Db 263 HSGKIVYRDLKLENLMDKOGHKITDPLGCKEGITDAATWKTFCGTPPYLAPEVLEND 322

Qy 181 YGRAVDMWGLGVVMYEMMCGRLPFYNQDHEKLFELIMEDIKFPRTLSDDAKSLLSGLLI 240

Db 323 YGRAVDMWGLGVVMYEMMCGRLPFYNQDHEKLFELIMEDIKFPRTLSDDAKSLLSGLLI 382

Qy 241 KDPNKRLOGGPPDDAKEINRHSFFSGVNWQDYDKLVPPFPQVTSSETDTRYFDEE 296

Db 383 KDPNKRLOGGPPDDAKEINRHSFFSGVNWQDYDKLVPPFPQVTSSETDTRYFDEE 438

RESULT 2

US-10-394-568-2

; Sequence 2, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUO, KUN
; APPLICANT: IVASHCHENKO, YURI
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; TITLE OF INVENTION: BY THE SERINE/THREONINE PROTEIN KINASE AKT
; FILE REFERENCE: A33990
; CURRENT APPLICATION NUMBER: US/10/394,568
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584,938
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-568-2

Query Match 100.0%; Score 1563; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFDYLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFDYLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 3
US-10-394-568-12
; Sequence 12, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUO, KUN
; APPLICANT: IVASHCHENKO, YURI
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; TITLE OF INVENTION: BY THE SERINE/THREONINE PROTEIN KINASE AKT
; FILE REFERENCE: A33990
; CURRENT APPLICATION NUMBER: US/10/394,568
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584,938
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-568-12

Query Match 100.0%; Score 1563; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFDYLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFDYLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 4
US-11-063-691-2
; Sequence 2, Application US/11063691
; Publication No. US20050142603A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/11/063,691
; CURRENT FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: US/09/526,043
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/125,108
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-063-691-2

Query Match 100.0%; Score 1563; DB 6; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFDYLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFDYLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 5
US-09-771-161A-246

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; Sequence 246, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-246

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 180
DB 263 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

RESULT 6
US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-247

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 180
DB 263 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

RESULT 7
US-09-771-161A-248
; Sequence 248, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 248
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 180
DB 263 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

RESULT 8
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 180
DB 263 HSGKIVYRDALKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYVQDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438
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US-10-394-322A-3
; Sequence 3, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT FILING DATE: 2003-03-20
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-3

Query Match      100.0%; Score 1563; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGYAMKILKKEVIIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGYAMKILKKEVIIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438

RESULT 9
US-10-217-574-33
; Sequence 33, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2002-05-01
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-574-33

Query Match      100.0%; Score 1563; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGYAMKILKKEVIIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGYAMKILKKEVIIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438
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Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 143 KTMNDFYLLKLGKGTGKVLVREKASGYAMKILKKEVIIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438

RESULT 10
US-10-217-555-33
; Sequence 33, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-33

Query Match      100.0%; Score 1563; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGYAMKILKKEVIIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGYAMKILKKEVIIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEIVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438
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RESULT 11

US-10-753-267-108
; Sequence 108, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriquez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003P1RQNMIM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-108

Query Match 100.0%; Score 1563; DB 5; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 202
QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYL 262
QY 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180
DB 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322
QY 181 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 240

DB 323 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 382
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

RESULT 12

US-09-526-043-17
; Sequence 17, Application US/09526043
; Publication No. US20030100049A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-526-043-17

Query Match 99.7%; Score 1558; DB 3; Length 454;
Best Local Similarity 99.7%; Pred. No. 4.9e-111;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 202
QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYL 262
QY 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180
DB 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322
QY 181 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 382
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

RESULT 13

US-11-063-691-17
; Sequence 17, Application US/11063691
; Publication No. US20050142603A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/11/063,691
; CURRENT FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: US/09/526,043
; PRIOR FILING DATE: 2000-03-14


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; PRIOR APPLICATION NUMBER: 60/125,108
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-11-063-691-17

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Db 143	KTWNDFYLLGLGFTGKVLVREKASGKYIYAMKILKKEVIIIAKDEVAHTLTESRVLKN	202		
Qy 61	TRHPFLTSLKYSFOTKORLCFVMEVWNGGELFPHLSRERVSEDRTPFYGAETVLSADYL	120		
Db 203	TRHPFLTSLKYSFOTKORLCFVMEVWNGGELFPHLSRERVSEDRTPFYGAETVLSADYL	262		
Qy 121	HSGKIVYRDULKLENMLDKOGHIKITDIFGLCKEGITDAAATMKTCGTPPEYLAPLEVDND	180		
Db 263	HSGKIVYRDULKLENMLDKOGHIKITDIFGLCKEGITDAAATMKTCGTPPEYLAPLEVDND	322		
Qy 181	YGRAVDNWGLGVVNYEMMCGRLPFVNODHEKLPFLILMEDIKFPRTLSDDAKSLLSGLLI	240		
Db 323	YGRAVDNWGLGVVNYEMMCGRLPFYNQDHEKLPFLILMEDIKFPRTLSDDAKSLLSGLLI	382		
Qy 241	KDPNKRILGGGDDAKEIMRHSFFSGVNWQDYYDKLVPPFPKQVTSSETDTRYPDEE	296		
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RESULT 14
US-10-116-722A-5
; Sequence 5, Application US/10116722A
; Publication No. US2003004496A1
; GENERAL INFORMATION:
; APPLICANT: LONGO, VALTER D.
; TITLE OF INVENTION: GENES, MUTATIONS, AND DRUGS THAT INCREASE CELLULAR
; TITLE OF INVENTION: RESISTANCE TO DAMAGE AND EXTEND LONGEVITY IN ORGANISMS
; TITLE OF INVENTION: FROM YEAST TO HUMANS
; FILE REFERENCE: 13761-7088
; CURRENT APPLICATION NUMBER: US/10/116.722A
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/281,213
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-116-722A-5

Query Match	89.2%	Score 1394.5	DB 4	Length 320
Best Local Similarity	87.8%	Pred. NO. 1.le-98		
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Db	189	YGRAVDW	GLGVVW	YEMMC	GR	LP	YNQD	HEK	FEL	IL	MEE	IR	PT	LG	PEAK	SL	248	
Qy	241	KD	NK	RL	G	G	G	P	D	A	K	E	T	M	R	H	S	296
Db	249	KD	T	Q	R	L	G	S	S	D	A	K	E	T	M	R	H	304

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RESULT 15
US-10-713-678-6
; Sequence 6, Application US/10713678
; Publication NO. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10713,678
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-713-678-6

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Query Match	89.2%	Score 1394.5	DB 4	Length 480
Best Local Similarity	87.8%	Pred. No. 1.7e-98		
Matches 260; Conservative	20	Mismatches 15	Indels 1	Gaps 1

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Db	146	TMBEFYLLKLGKGTGKVLVREKATGRYAMKILKEVILAKDEVAAHTLTESRVLQNS	205
Qy	62	RHPFLTSLKYSFOTKDRLCFVMEYVNGGELFFHLSRERVSESDTRFVGAIEVSALDYH	121
Db	206	RHPFLTALKYSFQTHDRLCFVMEYVNGGELFFHLSRERVSESDRARFVGAIEVSALDYH	265
Qy	122	SGK-IVYRDILKLENMLDKDGHIKITDFGLCKEGITDAAWTKTTCGTPPEYLAPLEVLEND	180
Db	266	SERNVYRDILKLENMLDKDGHIKITDFGLCKEGIKDGATWTKTFCGTPPEYLAPLEVLEND	325
Qy	181	YGRAVDWVGLGVVNYEMWCGRLFPYNQDHEKLPFLILMEDIKFPRTTSSDAKSLLSGLLI	240
Db	326	YGRAVDWVGLGVVNYEMWCGRLFPYNQDHEKLPFLILMEERFPRTTLCGPEAKSLLSGLLK	385
Qy	241	KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDYYDKLVPPFKPQVTSFDTDYFDBE	296
Db	386	KDPTQRLGGGSEDAKEMOHRFFANIVQDYYEKKLSPFPKPQVTSFDTDYFDBE	441

Search completed: February 13, 2006, 07:06:07
Job time : 282 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 13, 2006, 07:01:34 ; Search time 16 Seconds
(without alignments)
242.767 Million cell updates/sec

Title: US-10-601-311-1_COPY_143_438
Perfect score: 1563
Sequence: 1 KTMNDFYLLKLGKTFKVV.....VPPFKPQVTSYDTRYPDEE 296

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New: *
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1393.5	89.2	480	7	US-11-109-156-18	Sequence 18, Appl
2	856	54.8	543	6	US-10-821-234-1158	Sequence 1158, Ap
3	819.5	52.4	737	7	US-11-152-366-28	Sequence 28, Appl
4	761	48.7	942	6	US-10-770-726-76	Sequence 76, Appl
5	761	48.7	942	6	US-10-329-258-16	Sequence 16, Appl
6	758.5	48.5	351	7	US-11-099-958-2	Sequence 2, Appl
7	758.5	48.5	705	6	US-10-995-561-856	Sequence 856, App
8	758.5	48.5	706	6	US-10-995-561-855	Sequence 855, App
9	758.5	48.5	706	7	US-11-099-958-1	Sequence 1, Appl
10	735	47.0	495	6	US-10-770-726-81	Sequence 81, Appl
11	720	46.1	740	6	US-10-878-556A-129	Sequence 129, App
12	686.5	43.9	351	7	US-11-132-142-13	Sequence 13, Appl
13	680.5	43.5	343	7	US-11-092-168-3	Sequence 3, Appl
14	679.5	43.5	341	7	US-11-092-168-4	Sequence 4, Appl
15	675.5	43.2	351	7	US-11-132-142-14	Sequence 14, Appl
16	675.5	43.2	462	7	US-11-132-142-10	Sequence 10, Appl
17	669.5	42.8	350	6	US-10-497-767-4	Sequence 4, Appl
18	658.5	42.1	353	7	US-11-132-142-11	Sequence 11, Appl
19	656.5	42.0	395	7	US-11-132-142-12	Sequence 12, Appl
20	656.5	42.0	548	7	US-11-132-142-5	Sequence 5, Appl
21	650	41.6	398	7	US-11-132-142-7	Sequence 7, Appl
22	636.5	40.7	515	7	US-11-132-142-8	Sequence 8, Appl
23	634.5	40.6	381	7	US-11-132-142-9	Sequence 9, Appl
24	625.5	40.0	480	7	US-11-132-142-6	Sequence 6, Appl
25	571	36.5	256	6	US-10-877-346-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-11-109-156-18
; Sequence 18, Application US/1109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-Ichi Funahashi
; APPLICANT: Chitaki Senoo
; APPLICANT: Jun-Ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-18

26	571	36.5	256	7	US-11-113-424-183	Sequence 183, App
27	556	35.6	688	7	US-11-113-424-49	Sequence 49, Appl
28	555	35.5	688	7	US-11-113-424-48	Sequence 48, Appl
29	537	34.4	688	7	US-11-113-424-45	Sequence 45, Appl
30	529.5	33.9	756	7	US-11-113-837-20	Sequence 20, Appl
31	519.5	33.2	598	7	US-11-113-837-18	Sequence 18, Appl
32	517	33.1	689	7	US-11-113-424-47	Sequence 47, Appl
33	514	32.9	688	7	US-11-113-424-12	Sequence 12, Appl
34	514	32.9	689	7	US-11-113-424-46	Sequence 46, Appl
35	513.5	32.9	1663	6	US-10-055-877-148	Sequence 148, App
36	511.5	32.7	1732	6	US-10-055-877-147	Sequence 147, App
37	510.5	32.7	635	7	US-11-113-837-16	Sequence 16, App
38	507.5	32.5	637	7	US-11-113-837-4	Sequence 4, Appl
39	500.5	32.0	2053	6	US-10-877-346-11	Sequence 11, Appl
40	500.5	32.0	2066	6	US-10-877-346-9	Sequence 9, Appl
41	499.5	32.0	1590	6	US-10-055-877-146	Sequence 146, App
42	497	31.8	665	7	US-11-113-837-19	Sequence 19, Appl
43	493	31.5	1613	6	US-10-055-877-145	Sequence 145, App
44	493	31.5	1637	6	US-10-055-877-144	Sequence 144, App
45	491.5	31.4	396	7	US-11-125-295-11	Sequence 11, Appl

Query Match 89.2%; Score 1393.5; DB 7; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.7e-113;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TMNDPDKLLGKGTGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLNKT 61
Db 146 TMNEFEYLKLGKGTGKVLVREKATGRYYAMKILKEVIAKDEVAHTLTENRVLQNS 205

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYH 121
Db 206 RHPFLTALKYSFQTHDLRCFVMEYANGGELFFHLSRERFSEDRARFYGAIEVSALDYH 265

Qy 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBDND 180
Db 266 SEKNVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGMKTFCGTPPEYLAPEVLBDND 325

Qy 181 YGRAVDWMLGVVMEYMGCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLGLIK 240
Db 326 YGRAVDWMLGVVMEYMGCGRLPFYNQDHEKLFELIIMEEIRFPRTLGPPEAKSLLGLIK 385

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 386 KDPKQRLGGGSEDAKEIMQRRFFAGIVQHVYEXKLSPPFPKQVTSSETDTRYFDEE 441

RESULT 2
US-10-821-234-1158
; Sequence 1158, Application US/10821234
; Publication No. US200502551141
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462, 047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes version 1.0
; SEQ ID NO 1158
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1158

Query Match 54.8%; Score 856; DB 6; Length 543;
Best Local Similarity 54.8%; Pred. No. 7.8e-67;
Matches 161; Conservative 47; Mismatches 84; Indels 2; Gaps 2;

Qy 4 NDFPYLKLKGKGTGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRV-LKNTR 62
Db 208 SDFHFLKVIGKSGFKVLLARHKAEEFYAVKVLQKAILKKKEKHIMSERNVLLKNVK 267

Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYH 122
Db 268 HPFLVGLHFSQATKDLFVLDYINGGELFFHLQRECFUEPRARFYAAETASALGYH 327

Qy 123 GKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBDNDYG 182
Db 328 LNIYVYRDLEKLEMLDKDGHIKITDFGLCKENIEHNSTSTFCGTPPEYLAPEVLHKQPYD 387

Qy 183 RAVDWMLGVVMEYMGCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLGLIKD 242
Db 388 RTVDWMLGVVMEYMGCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLGLIKD 447

Qy 243 PNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 448 RTKRL-GAKDDFMEIKSHVFFSLINWDDLINKKTIPTTFNPNVSGNDLRHFDPE 500

RESULT 3
US-11-152-366-28
; Sequence 28, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

Query Match 52.4%; Score 819.5; DB 7; Length 737;
Best Local Similarity 50.0%; Pred. No. 1.7e-63;
Matches 150; Conservative 62; Mismatches 79; Indels 9; Gaps 3;

Qy 3 MNDFPYLKLKGKGTGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLNKTR 62
Db 405 LDFNFYKVLGSGFGKVMIAELKGDVYAVKVLQDDVDVCTWTEKRILALAR 464

Qy 63 -HPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYH 121
Db 465 KHPYLQLYCCFQTKDRLCFVMEYVNGGDLMFQIQSRKFEDEPRSRFYAAEVTLSALMFLH 524

Qy 122 SGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBDNDY 181
Db 525 QHGVYVYRDLEKLEMLDKDGHIKITDFGLCKEGILNGVTTTFCGTPDYIAPEILQBLEY 584

Qy 182 GRAVDWMLGVVMEYMGCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLGLIK 241
Db 585 GPSVDWMLGVVMEYMGCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLGLIK 644

Qy 242 DPNKRLLG-----GGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 645 NPHKRLGCVASQNGEDAIIQ---HPFFKEIDWVLLEQKIKPPFPKPRIKTRDWNVNDQD 701

RESULT 4
US-10-770-726-76
; Sequence 76, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 76
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-76

Query Match 48.7%; Score 761; DB 6; Length 942;
Best Local Similarity 48.0%; Pred. No. 2.7e-58;
Matches 143; Conservative 59; Mismatches 92; Indels 4; Gaps 2;

Qy	2	TW	N	D	F	D	F	Y	L	K	L	G	K	T	G	F	G	K	V	I	L	R	E	K	S	K	Y	I	A	M	K	I	L	K	E	V	I	I	A	K	O	E	V	A	H	T	L	T	S	R	V	L	---	58			
Db	611	T	L	E	D	K	F	L	A	V	I	G	R	H	G	F	G	K	V	I	L	R	E	K	S	K	Y	I	A	M	K	I	L	K	E	V	I	I	A	K	O	E	V	A	H	T	L	S	R	V	L	---	670				
Qy	59	K	N	T	R	P	F	L	T	S	L	K	Y	S	F	O	T	K	D	R	L	C	F	V	M	E	Y	N	G	G	L	F	P	H	L	S	R	E	R	F	V	S	D	R	T	F	Y	G	A	E	I	V	S	A	L	D	118
Db	671	T	S	A	G	H	P	L	V	N	L	F	C	F	O	T	P	E	H	C	F	V	M	E	Y	N	G	G	L	F	P	H	L	S	R	E	R	F	V	S	D	R	T	F	Y	G	A	E	I	V	S	A	L	D	729		
Qy	119	Y	L	H	S	K	I	V	R	D	L	K	N	L	M	L	D	K	D	G	H	I	K	I	T	D	F	L	C	K	E	G	I	T	D	A	A	T	M	K	T	F	C	G	T	P	E	L	A	P	E	V	L	D	178		
Db	730	F	L	H	E	K	I	V	R	D	L	K	N	L	M	L	D	T	E	G	Y	K	I	A	D	F	G	L	C	K	E	G	M	Y	G	D	R	T	S	T	F	C	G	T	P	E	L	A	P	E	V	L	D	789			
Qy	179	N	D	Y	G	R	A	V	D	W	G	L	V	Y	E	M	M	C	R	L	P	F	Y	N	Q	D	H	B	K	L	F	E	L	I	M	E	D	I	K	P	R	T	L	S	S	D	A	K	S	L	L	S	G	238			
Db	790	T	S	Y	T	R	A	V	D	W	G	L	V	Y	E	M	L	V	G	E	S	P	F	P	G	D	D	E	E	V	F	D	S	I	N	D	E	V	R	P	R	F	L	S	A	E	A	I	G	I	M	R	L	849			
Qy	239	L	I	K	D	N	K	R	L	G	G	G	P	D	A	K	E	I	M	R	H	S	F	S	G	V	N	Q	D	Y	K	L	V	P	P	K	P	Q	V	T	S	T	D	T	R	Y	F	D	E	296							
Db	850	L	R	N	P	E	R	L	G	S	E	R	D	A	E	V	K	P	F	T	L	G	E	A	L	L	R	P	P	P	V	P	T	L	S	G	R	T	D	V	S	N	D	E	F	907											

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RESULT 5
US-10-329-258-16
; Sequence 16, Application US/10329258
; Publication No. US20060024233A1
; GENERAL INFORMATION:
; APPLICANT: MUELLER, SABINE
; APPLICANT: GONZALEZ-ZULUETA, MIRELLA
; APPLICANT: FOEHR, ERIK
; APPLICANT: CHIN, DANIEL J.
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION OF
; FILE REFERENCE: AGYT-008US2
; CURRENT APPLICATION NUMBER: US/10/329,258
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/343,422
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-329-258-16

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RESULT 6
US-11-099-958-2
; Sequence 2, Application US/11099958
; Publication No. US20060003431A1

```

; GENERAL INFORMATION:
; APPLICANT: Xu, Zhand Bao
; APPLICANT: Olland, Stephane
; APPLICANT: Wolfrom, Scott
; APPLICANT: Malakian, Karl
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Lee, Julie
; APPLICANT: Fitz, Lori
; APPLICANT: Greco, Rita
; APPLICANT: Chaudhary, Divya
; APPLICANT: Somers, William Stuart
; APPLICANT: Mosyak, Lidia
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
; FILE REFERENCE: 16163-018001
; CURRENT APPLICATION NUMBER: US/11/099,958
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/560,441
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-099-958-2

```

```

RESULT 7
US-10-995-561-856
; Sequence 856, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995.561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 856
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-856

```

RESULT 6

```
Best Local Similarity 48.5%; Pred. No. 3.1e-58;
Matches 143; Conservative 54; Mismatches 93; Indels 5; Gaps 2;

Qy 3 MNDFDYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT- 61
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
376 IEDFILHKLKLGSGFGKVLAEFKTNQFFAIKALKDDVLMDDDDVECTWVEKRVLSLAW 435
Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSERDTRFRYGAEIVSALDYH 121
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
436 EHPFLTHMCTFQTKENLFFVMEYVNGGDLMYHQSCHKFDLSRATFYAAEIIIGLQFLH 495
Qy 122 SGKIVYRDLENLMLDKDGHKITDGLCKEGITDAATMKTFCGTPYLAPEVLENDY 181
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
496 EHPFLTHMCTFQTKENLFFVMEYVNGGDLMYHQSCHKFDLSRATFYAAEIIIGLQFLH 555
Qy 182 GRAYDWMGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSGLLIK 241
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
556 NHSVDWMSFGVLLIYEMLIGQSPFHGQDEEELFHSIRMDNPFYPRWLEKEAKDLLVLFVR 615
Qy 242 DPNKRLGGPPDDAKEIMRHSFFSGVNWQVVDKLVPPFPKQVTSSETDTRYFDEE 296
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
616 EPEKRLGVRGD----IRQHPLFREINWEELERKEIDPPFRPKVKSPPDCSNFDKE 666

RESULT 8
US-10-995-561-855
; Sequence 855, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 855
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-855

Query Match 48.5%; Score 758.5; DB 6; Length 706;
Best Local Similarity 48.5%; Pred. No. 3.1e-58;
Matches 143; Conservative 54; Mismatches 93; Indels 5; Gaps 2;

Qy 3 MNDFDYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT- 61
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 IEDFILHKLKLGSGFGKVLAEFKTNQFFAIKALKDDVLMDDDDVECTWVEKRVLSLAW 436
Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSERDTRFRYGAEIVSALDYH 121
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
437 EHPFLTHMCTFQTKENLFFVMEYVNGGDLMYHQSCHKFDLSRATFYAAEIIIGLQFLH 496
Qy 122 SGKIVYRDLENLMLDKDGHKITDGLCKEGITDAATMKTFCGTPYLAPEVLENDY 181
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
497 SGKIVYRDLENLMLDKDGHKITDGLCKEGITDAATMKTFCGTPYLAPEVLENDY 556
Qy 182 GRAYDWMGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSGLLIK 241
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
557 NHSVDWMSFGVLLIYEMLIGQSPFHGQDEEELFHSIRMDNPFYPRWLEKEAKDLLVLFVR 616
Qy 242 DPNKRLGGPPDDAKEIMRHSFFSGVNWQVVDKLVPPFPKQVTSSETDTRYFDEE 296
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
617 EPEKRLGVRGD----IRQHPLFREINWEELERKEIDPPFRPKVKSPPDCSNFDKE 667
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```
RESULT 9
US-11-099-958-1
; Sequence 1, Application US/11099958
; Publication No. US20060003431A1
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```
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhang Bao
; APPLICANT: Olland, Stephanie
; APPLICANT: Wolfrom, Scott
; APPLICANT: Malakian, Karl
; APPLICANT: Lin, Laura
; APPLICANT: Lee, Julie
; APPLICANT: Stahl, Lori
; APPLICANT: Greco, Rita
; APPLICANT: Chaudhary, Divya
; APPLICANT: Somers, William Stuart
; APPLICANT: Mosyak, Lidia
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
; FILE REFERENCE: 16163-018001
; CURRENT APPLICATION NUMBER: US/11/099,958
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/560,441
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-099-958-1

Query Match 48.5%; Score 758.5; DB 7; Length 706;
Best Local Similarity 48.5%; Pred. No. 3.1e-58;
Matches 143; Conservative 54; Mismatches 93; Indels 5; Gaps 2;

Qy 3 MNDFDYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT- 61
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 IEDFILHKLKLGSGFGKVLAEFKTNQFFAIKALKDDVLMDDDDVECTWVEKRVLSLAW 436
Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSERDTRFRYGAEIVSALDYH 121
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
437 EHPFLTHMCTFQTKENLFFVMEYVNGGDLMYHQSCHKFDLSRATFYAAEIIIGLQFLH 496
Qy 122 SGKIVYRDLENLMLDKDGHKITDGLCKEGITDAATMKTFCGTPYLAPEVLENDY 181
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
497 SGKIVYRDLENLMLDKDGHKITDGLCKEGITDAATMKTFCGTPYLAPEVLENDY 556
Qy 182 GRAYDWMGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSGLLIK 241
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
557 NHSVDWMSFGVLLIYEMLIGQSPFHGQDEEELFHSIRMDNPFYPRWLEKEAKDLLVLFVR 616
Qy 242 DPNKRLGGPPDDAKEIMRHSFFSGVNWQVVDKLVPPFPKQVTSSETDTRYFDEE 296
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
617 EPEKRLGVRGD----IRQHPLFREINWEELERKEIDPPFRPKVKSPPDCSNFDKE 667

RESULT 10
US-10-770-726-81
; Sequence 81, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-81
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; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-092-168-3
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Query Match 43.5%; Score 580.5; DB 7; Length 343;
Best Local Similarity 44.4%; Pred. No. 7.1e-52;
Matches 131; Conservative 53; Mismatches 104; Indels 7; Gaps 2;
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Qy 3 MNDPDKLLKLGKTFGKIVLVREKASGYAMKILKEVIIAKDEVAHTLTESVLRNTR 62
Db 33 LDQPERIKTLTGSGFGRVLMVKHETGNHFAKILDKQKVVKLQIETHLNEKRILQAVN 92
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFESDRTRFYGAETVSALDYLS 122
Db 93 PFPLVKLEYSFKNSNLYMWYVPGGEMFSLHRIGRFSEPHARFYAAQIVLTFEYLHS 152
Qy 123 GKIVYRDLKLENLMDKDGHIKITDFGLCK--EGITDAATMKTCFCTPEYLAPEVLEND 180
Db 153 LDLIYRDLKPENLIDQGYIQVTDGFAKRVKGR-----WTLCTGPEYLAPEIILSKG 207
Qy 181 YGRAVDWMLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGILLI 240
Db 208 YNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFFSHFSSDLKOLLRLNQ 267
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPPKPQVTSSETDTRYFDE 295
Db 268 VDLTKRFGNLKGVNDIKNHNKWFATTDWIAIYQKRVKVEAPFIPKFGPGDTSNFDD 322
```

```
RESULT 14
US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bears, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4
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Query Match 43.5%; Score 679.5; DB 7; Length 341;
Best Local Similarity 44.4%; Pred. No. 8.7e-52;
Matches 131; Conservative 53; Mismatches 104; Indels 7; Gaps 2;

Qy 3 MNDPDKLLKLGKTFGKIVLVREKASGYAMKILKEVIIAKDEVAHTLTESVLRNTR 62
Db 31 LDQPERIKTLTGSGFGRVLMVKHESGNHYAMKILDKQKVVKLQIETHLNEKRILQAVN 90
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFESDRTRFYGAETVSALDYLS 122
Db 91 PFPLVKLEFSFKNSNLYMWYVAGGEMFSLHRIGRFAEPHARFYAAQIVLTFEYLHS 150
Qy 123 GKIVYRDLKLENLMDKDGHIKITDFGLCK--EGITDAATMKTCFCTPEYLAPEVLEND 180
Db 151 LDLIYRDLKPENLIDQGYIQVTDGFAKRVKGR-----WTLCTGPEYLAPEIILSKG 205
Qy 181 YGRAVDWMLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGILLI 240
Db 206 YNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFFSHFSSDLKOLLRLNQ 265
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPPKPQVTSSETDTRYFDE 295
Db 266 VDLTKRFGNLKGVNDIKNHNKWFATTDWIAIYQKRVKVEAPFIPKFGPGDTSNFDD 320
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```
RESULT 15
US-11-132-142-14
; Sequence 14, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-142-14
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```
Query Match 43.2%; Score 675.5; DB 7; Length 351;
Best Local Similarity 44.1%; Pred. No. 2e-51;
Matches 130; Conservative 54; Mismatches 104; Indels 7; Gaps 2;

Qy 3 MNDPDKLLKLGKTFGKIVLVREKASGYAMKILKEVIIAKDEVAHTLTESVLRNTR 62
Db 41 LDQPERIKTLTGSGFGRVLMVKHETGNHYAMKILDKQKVVKLQIETHLNEKRILQAVN 100
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFESDRTRFYGAETVSALDYLS 122
Db 101 PFPLVKLEFSFKNSNLYMWYVPGGEMFSLHRIGRFSEPHARFYAAQIVLTFEYLHS 160
Qy 123 GKIVYRDLKLENLMDKDGHIKITDFGLCK--EGITDAATMKTCFCTPEYLAPEVLEND 180
Db 161 LDLIYRDLKPENLIDQGYIQVTDGFAKRVKGR-----WTLCTGPEYLAPEIILSKG 215
Qy 181 YGRAVDWMLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGILLI 240
Db 216 YNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFFSHFSSDLKOLLRLNQ 275
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPPKPQVTSSETDTRYFDE 295
Db 276 VDLTKRFGNLKGVNDIKNHNKWFATTDWIAIYQKRVKVEAPFIPKFGPGDTSNFDD 330
```


Search completed: February 13, 2006, 07:06:26
Job time : 17 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 13, 2006, 06:28:06 ; Search time 309 Seconds

(without alignment)
420.894 Million cell updates/sec

Title: US-10-601-311-1_COPY_143_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFGKV.....VPPFKPQVTSDFRYFDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Genesep21:*
- 1: Genesep1980s:*
- 2: Genesep1990s:*
- 3: Genesep2000s:*
- 4: Genesep2001s:*
- 5: Genesep2002s:*
- 6: Genesep2003as:*
- 7: Genesep2003bs:*
- 8: Genesep2004s:*
- 9: Genesep2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563	100.0	465	3 AAB19011	Aab19011 Amino aci
2	1563	100.0	465	4 AAG78018	Aag78018 Human Act
3	1563	100.0	465	4 AAB19996	Aab19996 Human ser
4	1563	100.0	465	4 AAB19998	Aab19998 Human ser
5	1563	100.0	465	8 ADG85255	Adg85255 Human Chr
6	1563	100.0	465	8 ADG85245	Adg85245 Human Chr
7	1563	100.0	479	3 AAB19284	Aab19284 Amino aci
8	1563	100.0	479	3 AAB13393	Aab13393 Human Akt
9	1563	100.0	479	5 AAU79420	Aau79420 Human pro
10	1563	100.0	479	5 ABB06998	Abb06998 Human Akt
11	1563	100.0	479	6 ABR57474	Abt57474 Human PKB
12	1563	100.0	479	7 ADf45034	Adf45034 Human kin
13	1563	100.0	479	8 ADN71940	Adn71940 Human ser
14	1563	100.0	479	8 ADQ88266	Adq88266 Human 141
15	1558	99.7	454	4 AAG78021	Aag78021 Akt3 rela
16	1555	99.5	479	3 AAB43132	Aab43132 Human ORF
17	1466	93.8	319	4 AAB99833	Aab99833 AGC prote
18	1466	93.8	319	4 ADJ38881	Adj38881 PKBgamma
19	1420.5	90.9	480	8 ADN71942	Adn71942 Chicken s
20	1394.5	89.2	479	2 AAU03453	Aau03453 Mouse c-A
21	1394.5	89.2	480	3 AAY92223	Aay92223 Wild type
22	1394.5	89.2	480	5 AAE17784	Aae17784 Mouse Akt
23	1394.5	89.2	501	2 AAW03452	Aaw03452 Mouse v-A
24	1394.5	89.2	517	8 ADL25357	Adl25357 ARKS rela

25	1393.5	89.2	480	2 AAW17972	Aaw17972 Human RAC
26	1393.5	89.2	480	2 AAW17984	Aaw17984 Human RAC
27	1393.5	89.2	480	2 AAW18515	Aaw18515 Human RAC
28	1393.5	89.2	480	2 AAY52706	Aay52706 Human Akt
29	1393.5	89.2	480	2 AAY33999	Aay33999 Human Akt
30	1393.5	89.2	480	2 ADf77614	Adf77614 Human Akt
31	1393.5	89.2	480	3 AAY92221	Aay92221 Wild type
32	1393.5	89.2	480	4 AAG78020	Aag78020 Human Akt
33	1393.5	89.2	480	4 AAG67620	Aag67620 Amino aci
34	1393.5	89.2	480	4 AAG67441	Aag67441 Amino aci
35	1393.5	89.2	480	5 AAU79418	Aau79418 Human pro
36	1393.5	89.2	480	5 AAE17782	Aae17782 Human Akt
37	1393.5	89.2	480	5 ABB06996	Abb06996 Human Akt
38	1393.5	89.2	480	6 ABR57472	Abt57472 Human PKB
39	1393.5	89.2	480	7 ADf18630	Adf18630 Human Akt
40	1393.5	89.2	480	7 ADf45032	Adf45032 Human kin
41	1393.5	89.2	480	8 ADL25355	Adl25355 Human ARK
42	1393.5	89.2	480	8 ADO22518	Ado22518 Biochemic
43	1393.5	89.2	480	8 ADQ37844	Adq37844 Human pho
44	1393.5	89.2	480	8 ADR06338	Adr06338 IRK-1 pro
45	1393.5	89.2	480	8 AEM81592	Aem81592 Tumour-as

ALIGNMENTS

RESULT 1	
AAB19011	
ID	AAB19011 standard; protein; 465 AA.
XX	AC AAB19011;
XX	XX
DT	08-FEB-2001 (first entry)
XX	XX
DE	Amino acid sequence of a human Akt3 polypeptide.
XX	XX
KW	Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;
KW	hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;
KW	reperfusion injury; myocardial ischemia reperfusion injury; stroke;
KW	liver damage; renal failure; organ transplantation; coronary artery.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WO200056866-A2.
XX	XX
PD	28-SEP-2000.
XX	XX
PF	14-MAR-2000; 2000WO-US006574.
XX	XX
PR	19-MAR-1999; 99US-0125108P.
XX	XX
PA	(AVET) AVENTIS PHARM PROD INC.
XX	XX
PI	Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
XX	XX
DR	WPI; 2000-638260/61.
DR	N-P5DB; AAA96637.
XX	XX
PT	Novel AKT3 nucleic acid and proteins capable of preventing apoptotic cell
PT	death induced by apoptosis stimulating kinase 1 useful for treating
XX	XX
PS	myocardial infarction or ischemia reperfusion injury.
XX	XX
CC	Claim 16; Page 64-65; 73pp; English.
XX	XX
CC	The present sequence represents a human Akt3 protein. Expression of Akt3
CC	prevents apoptotic cell death induced by apoptotic stimulating kinase 1
CC	(ASK1). The Akt3 polypeptide is useful for inhibiting cell death,
CC	preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or
CC	necrosis in a patient suffering from myocardial infarction or ischemia
CC	reperfusion injury. The polypeptide is also useful for treating
CC	myocardial infarction or ischemia reperfusion injury, where the
CC	reperfusion injury is myocardial ischemia reperfusion injury or is
CC	associated with stroke, liver damage, renal failure, organ

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CC transplantation or coronary artery by pass grafting
XX Sequence 465 AA;
SQ
    Query Match      100.0%; Score 1563; DB 3; Length 465;
    Best Local Similarity 100.0%; Pred. No. 1.1e-155;
    Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFDYLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFDYLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDYYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDYYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 2
AAG78018
ID AAG78018 standard; protein; 465 AA.
XX
AC AAG78018;
XX
DT 31-JAN-2002 (first entry)
XX
DE Human Akt3.
XX
KW Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;
KW cerebroprotective; neurotropic; hepatotrophic; antiarthritic;
KW osteopathic; vasotropic; hepatotrophic; inhibitor of apoptosis; ASK1;
KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;
KW ischaemia reperfusion injury; stroke; organ transplantation;
KW coronary artery bypass; tumour cell survival; gene therapy;
KW Alzheimer's disease; osteoarthritis.
XX
OS Homo sapiens.
XX
PN WO200168850-A2.
XX
PD 20-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-US007663.
XX
PR 14-MAR-2000; 2000US-00526043.
XX
PA (AVET ) AVENTIS PHARM PROD INC.
XX
PI Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
XX
XX WPI; 2001-582452/65.
XX
DR N-PSDB; AAH79025.
XX
PT New nucleic acid encoding human Akt3 protein, useful for inhibiting cell
PT death and treating myocardial infarction, ischemia reperfusion injury
PT associated with stroke, liver damage and renal failure.
XX
PS Claim 17; Fig 1; 73pp; English.
XX
CC The invention relates to human Akt3 protein (AH/PH-domain containing
CC serine/threonine kinase, Akt) comprising a fully defined sequence
CC (AAG78018) of 465 amino acids, its splice variant or allelic variant,
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CC where the encoding polynucleotide hybridises under stringent conditions
CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570
CC base pairs defined in the specification. Akt3 has cerebroprotective,
CC neurotropic, hepatotrophic, antiarthritic, osteopathic, vasotropic and
CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis
CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a
CC regulatory region is useful for inhibiting cell death in cardiac myocytes
CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial
CC infarction or ischaemia reperfusion injury, particularly that associated
CC with stroke, liver damage, renal failure, organ transplantation or
CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving
CC Akt3 activity during treatment of patients suffering from myocardial
CC infarction or ischaemia reperfusion injury and inhibitors of Akt3
CC activity decrease tumour cell survival and result in tumour regression.
CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the
CC quantity of cell death and final infarct size, resulting in improved post
CC -infarction function, improved quality of life and reduced mortality. In
CC patients with existing heart failure, gene therapy with Akt3 retards the
CC process of ventricular dilation and slows down disease progression. Akt3
CC gene therapy is useful for treating other disease states, involving cell
CC death by apoptosis, including Alzheimer's disease, liver degeneration or
CC osteoarthritis.
XX
SQ Sequence 465 AA;
    Query Match      100.0%; Score 1563; DB 4; Length 465;
    Best Local Similarity 100.0%; Pred. No. 1.1e-155;
    Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFDYLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFDYLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTCGTPPEYLAPEVLEDND 180
Db 263 HSGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTCGTPPEYLAPEVLEDND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDYYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDYYDKLVPPFPKQVTSSETDTRYFDEE 438
```

```
RESULT 3
AAB19996
ID AAB19996 standard; protein; 465 AA.
XX
AC AAB19996;
XX
DT 28-MAR-2001 (first entry)
XX
DE Human serine/threonine protein kinase Akt3.
XX
KW Akt3; human; protein kinase; vascular endothelial growth factor; VEGF;
KW inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO200077190-A2.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US015098.
XX
XX 11-JUN-1999; 99US-0138724P.
PR 03-NOV-1999; 99GB-00026058.
```

```
XX PA (AVET ) AVENTIS PHARM PROD INC.
XX PI Guo K, Ivashchenko Y, Clark K;
XX DR WPI; 2001-025336/03.
XX DR N-PSDB; AAA89264.
XX XX
XX PT Inducing expression of vascular endothelial growth factor, useful for
XX PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal
XX PT ischemia or pulmonary ischemia, comprises administering a
XX PT serine/threonine protein kinase Akt protein.
XX XX
XX PS Example 1; Page 58-59; 67pp; English.
XX XX
XX CC The present sequence is that of human Akt3, a novel Akt isoform. Akt3 is
XX CC a serine/threonine protein kinase capable of inducing vascular
XX CC endothelial growth factor (VEGF) expression. The sequence was deduced
XX CC from cDNA (see AAA89264) isolated from a heart cDNA library. Akt3 is
XX CC shorter than Akt1 (see AAB19997) and Akt2 (see AAB19998) and there is no
XX CC significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of
XX CC the molecules. A claimed method of inducing expression of VEGF in a cell
XX CC involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding
XX CC such a protein. The cell is preferably from a patient suffering from an
XX CC ischaemic condition, especially cerebrovascular, renal, pulmonary, limb
XX CC or myocardial ischaemia, or ischaemic, idiopathic or hypertrophic
XX CC cardiomyopathy. The result is beneficial collateral blood vessel
XX CC formation. A claimed method of inhibiting angiogenesis in a patient
XX CC suffering from a tumour, comprises inhibiting the level of Akt activity
XX CC in the patient, thereby inhibiting production of VEGF. The method
XX CC comprises introducing an Akt antisense nucleic acid, an intracellular
XX CC binding protein (e.g. a scfv) that specifically binds the Akt protein, or
XX CC a nucleic acid encoding a dominant negative form of an Akt
XX SQ Sequence 465 AA;

Query Match 100.0%; Score 1563; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.le-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 120
DB 203 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 262

QY 121 HSGKIVYRDLEKLEMLDKDGHKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 322

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSLGLLI 240
DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSLGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRFYDSE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRFYDSE 438

RESULT 4
AAB19998
ID AAB19998 standard; protein; 465 AA.
XX AAB19998;
AC AAB19998;
XX XX
XX DT 28-MAR-2001 (first entry)
XX XX
XX DE Human serine/threonine protein kinase Akt2.
XX KW Akt2; human; protein kinase; vascular endothelial growth factor; VEGF;
XX inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; therapy.
```

```
XX OS Homo sapiens.
XX PN WO200077190-A2.
XX PD 21-DEC-2000.
XX XX
XX PF 01-JUN-2000; 2000WO-US015098.
XX PR 11-JUN-1999; 99US-0138724P.
XX PR 03-NOV-1999; 99GB-00026058.
XX XX
XX PA (AVET ) AVENTIS PHARM PROD INC.
XX XX
XX PI Guo K, Ivashchenko Y, Clark K;
XX XX
XX DR WPI; 2001-025336/03.
XX XX
XX PT Inducing expression of vascular endothelial growth factor, useful for
XX PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal
XX PT ischemia or pulmonary ischemia, comprises administering a
XX PT serine/threonine protein kinase Akt protein.
XX XX
XX PS Disclosure; Page 63-64; 67pp; English.
XX XX
XX CC The present sequence is that of human Akt2, a serine/threonine protein
XX CC kinase capable of inducing vascular endothelial growth factor (VEGF)
XX CC expression. A claimed method of inducing expression of VEGF in a cell
XX CC involves administering Akt2, Akt1 (see AAB19997) or Akt3 (see AAB19996),
XX CC or a nucleic acid encoding such a protein. The cell is preferably from a
XX CC patient suffering from an ischaemic condition, especially
XX CC cerebrovascular, renal, pulmonary, limb or myocardial ischaemia, or
XX CC ischaemic, idiopathic or hypertrophic cardiomyopathy. The result is
XX CC beneficial collateral blood vessel formation. A claimed method of
XX CC inhibiting angiogenesis in a patient suffering from a tumour, comprises
XX CC inhibiting the level of Akt activity in the patient, thereby inhibiting
XX CC production of VEGF. The method comprises introducing an Akt antisense
XX CC nucleic acid, an intracellular binding protein (e.g. a scfv) that
XX CC specifically binds the Akt protein, or a nucleic acid encoding a dominant
XX CC negative form of an Akt
XX SQ Sequence 465 AA;

Query Match 100.0%; Score 1563; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.le-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 120
DB 203 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIEVSALDYL 262

QY 121 HSGKIVYRDLEKLEMLDKDGHKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 322

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSLGLLI 240
DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSLGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRFYDSE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRFYDSE 438

RESULT 5
ADG85255
ID ADG85255 standard; protein; 465 AA.
XX ADG85255;
AC ADG85255;
```

XX 25-MAR-2004 (first entry)
DT Human Chrysoosporium associated protein #3.
DE beta-glucosidic bond; beta-xylosidic bond; human.
XX Homo sapiens.
OS US2004002136-A1.
XX 01-JAN-2004.
PD 21-MAR-2003; 2003US-00394568.
XX 06-OCT-1998; 98WO-EP006496.
PR 06-OCT-1999; 99WO-NL000618.
PR 13-APR-2000; 2000US-00548938.
XX (EMAL//) EMALFARB M A.
PA (BURL//) BURLINGAME R P.
PA (OLSO//) OLSON P T.
PA (SINI//) SINITSYN A P.
PA (PARR//) FARRICHE M.
PA (BOUS//) BOUSSON J C.
PA (PYN//) PYNNONEN C M.
PA (PUNT//) PUNT P J.
PA (VZEI//) VAN ZEIJL C M J.
XX Emalfarb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parriche M;
PI Bousson JC, Pynnonen CM, Punt PJ, Van Zeijl CMJ;
XX WPI; 2004-061663/06.
XX Novel mutant Chrysoosporium strain comprising nucleic acid sequence
PT encoding polypeptide of interest such as proteases and lipases, the
PT nucleic acid sequence being operably linked to expression-regulating
PT region.
XX Disclosure; SEQ ID NO 12; 70pp; English.
XX The invention relates to a mutant Chrysoosporium strain comprising a
CC nucleic acid sequence encoding a polypeptide of interest. A mutant
CC Chrysoosporium strain is useful for producing a polypeptide of interest by
CC culturing a mutant Chrysoosporium strain under conditions permitting
CC expression of the protein or polypeptide, and recovering the subsequently
CC produced polypeptide of interest. The conditions further permit secretion
CC of the protein or polypeptide of interest. The polypeptides are useful
CC for hydrolysing beta-glucosidic bonds. A polypeptide is useful for
CC hydrolysing beta-xylosidic bonds. The present sequence represents a human
CC Chrysoosporium associated protein.
XX Sequence 465 AA;
Query Match 100.0%; Score 1563; DB 8; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.1e-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTSSRLKN 60
Db 143 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTSSRLKN 202
Qy 61 TRHPFLTSKYSFQTKDRLCFMVEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSKYSFQTKDRLCFMVEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 262
Qy 121 HSGKIVYRDLEKLEMLDKDGHKITDGLCKEGITDAATMKTCGTPPEYLAPVLEDND 180
Db 263 HSGKIVYRDLEKLEMLDKDGHKITDGLCKEGITDAATMKTCGTPPEYLAPVLEDND 322
Qy 181 YGRAVDWVGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSDDAKSLISGLLI 240
Db 323 YGRAVDWVGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSDDAKSLISGLLI 382

Qy 241 KDPNKRLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSTDTRYFDEE 296
Db 383 KDPNKRLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSTDTRYFDEE 438
RESULT 6
ADG85245
ID ADG85245 standard; protein; 465 AA.
XX AC ADG85245;
XX DT 25-MAR-2004 (first entry)
XX DE Human Chrysoosporium associated protein #1.
XX KW beta-glucosidic bond; beta-xylosidic bond; human.
XX OS Homo sapiens.
XX PN US2004002136-A1.
XX PD 01-JAN-2004.
XX PF 21-MAR-2003; 2003US-00394568.
XX PR 06-OCT-1998; 98WO-EP006496.
PR 06-OCT-1999; 99WO-NL000618.
PR 13-APR-2000; 2000US-00548938.
XX (EMAL//) EMALFARB M A.
PA (BURL//) BURLINGAME R P.
PA (OLSO//) OLSON P T.
PA (SINI//) SINITSYN A P.
PA (PARR//) PARRICHE M.
PA (BOUS//) BOUSSON J C.
PA (PYN//) PYNNONEN C M.
PA (PUNT//) PUNT P J.
PA (VZEI//) VAN ZEIJL C M J.
XX Emalfarb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parriche M;
PI Bousson JC, Pynnonen CM, Punt PJ, Van Zeijl CMJ;
XX WPI; 2004-061663/06.
XX N-PSDB; ADG85244.
XX Novel mutant Chrysoosporium strain comprising nucleic acid sequence
PT encoding polypeptide of interest such as proteases and lipases, the
PT nucleic acid sequence being operably linked to expression-regulating
PT region.
XX Disclosure; SEQ ID NO 2; 70pp; English.
XX The invention relates to a mutant Chrysoosporium strain comprising a
CC nucleic acid sequence encoding a polypeptide of interest. A mutant
CC Chrysoosporium strain is useful for producing a polypeptide of interest by
CC culturing a mutant Chrysoosporium strain under conditions permitting
CC expression of the protein or polypeptide, and recovering the subsequently
CC produced polypeptide of interest. The conditions further permit secretion
CC of the protein or polypeptide of interest. The polypeptides are useful
CC for hydrolysing beta-glucosidic bonds. A polypeptide is useful for
CC hydrolysing beta-xylosidic bonds. The present sequence represents a human
CC Chrysoosporium associated protein.
XX Sequence 465 AA;
Query Match 100.0%; Score 1563; DB 8; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.1e-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTSSRLKN 60
Db 143 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTSSRLKN 202

QY 61 TRHPFLTSKYSFQTKORLCFVMEYVNGGELFFHLSRERVSFSDRTFRYGAEIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKORLCFVMEYVNGGELFFHLSRERVSFSDRTFRYGAEIVSALDYL 262
QY 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATWKTCGTPPEYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATWKTCGTPPEYLAPEVLEND 322
QY 181 YGRAVDWMLGVLVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMLGVLVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
QY 241 KDPNKRLLGGGPDDAKEIMRHSFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 438
RESULT 7
AAB19284
ID AAB19284 standard; protein; 479 AA.
AC AAB19284;
XX
XX 19-FEB-2001 (first entry)
DE Amino acid sequence of a human kinase B-gamma polypeptide.
XX Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;
KW phosphoinositide 3-kinase; insulin signalling;
KW pleckstrin homology domain.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Modified-site 305 /note= "active phosphorylation site"
FT Modified-site 472 /note= "putative phosphorylation site"
FT
XX WO200058446-A1.
XX
XX 05-OCT-2000.
XX
XX 23-MAR-2000; 2000WO-SE000571.
XX
XX 25-MAR-1999; 99SE-00001115.
XX (PHAA) PHARMACIA & UPJOHN AB.
XX
XX Attersand A;
XX
XX WPI: 2000-647230/62.
XX N-PSDB; AAC61592.
XX
XX Novel human protein kinase B gamma polynucleotides and polypeptides
PT useful as probe or primers in polymerase chain reaction and to raise
PT antibodies useful in diagnostic assays for detecting polypeptide
PT expression.
XX
XX Claim 8; Page 19-20; 27pp; English.
XX
XX The present sequence represents a human protein kinase B gamma (PKB)
CC polypeptide. PKB is activated by insulin or insulin growth factor 1.
CC Lipid products of phosphoinositide 3-kinase act in insulin signalling by
CC binding to pleckstrin homology domains of PKB. PKB polynucleotides may be
CC used as a source of probes and primers. PKB polypeptides are used to
CC raise antibodies, which are used in diagnostic assays. The polypeptides
CC are also useful for screening for compounds which affect insulin
XX signalling pathways
XX
XX Sequence 479 AA;
SQ

Query Match 100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.2e-155; Indels 0; Gaps 0;
Matches 296; Conservative 0; Mismatches 0;
QY 1 KTMNDFDYLLKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFDYLLKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202
QY 61 TRHPFLTSKYSFQTKORLCFVMEYVNGGELFFHLSRERVSFSDRTFRYGAEIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKORLCFVMEYVNGGELFFHLSRERVSFSDRTFRYGAEIVSALDYL 262
QY 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATWKTCGTPPEYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATWKTCGTPPEYLAPEVLEND 322
QY 181 YGRAVDWMLGVLVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMLGVLVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
QY 241 KDPNKRLLGGGPDDAKEIMRHSFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 438
RESULT 8
AAB13393
ID AAB13393 standard; protein; 479 AA.
AC AAB13393;
XX
XX 13-NOV-2000 (first entry)
DE Human Akt-3.
XX Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytostatic;
KW apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
KW chromosome 1q43-44.
XX Homo sapiens.
XX WO200037613-A2.
XX
XX 29-JUN-2000.
XX
XX 17-DEC-1999; 99WO-GB004311.
XX
XX 22-DEC-1998; 98GB-00028375.
XX (JANC) JANSSEN PHARM NV.
XX
XX Masure SLJ, Richardson A;
XX
XX WPI: 2000-498840/44.
XX N-PSDB; AAA62450, AAA62451.
XX
XX New human serine/threonine kinase protein and the polynucleotide encoding
PT the protein, useful for preparing a medicament for treating disorders
PT associated with human serine/threonine kinase protein activity,
PT especially cancer.
XX
XX Claim 6; Fig 1; 61pp; English.
XX
XX The present sequence is human Akt-3. Akt-3 is a third human isoform of
CC Akt, which is also known as protein kinase B (PKB) or "related to A and C
CC protein kinase" (RAC-PK). It is located on human chromosome 1, region q43
CC -q44. A human hippocampal EST sequence that showed high similarity to the
CC rat RAC-PKgamma sequence was used to design primers for 3' rapid
CC amplification of cDNA ends (3' RACE). The sequence obtained in the first
CC round of 3' RACE was used to design primers for a second round. The
CC complete sequence was then amplified from human hippocampal cDNA by PCR
CC using primers based on the product of the second round of 3' RACE. Akt
CC can inhibit apoptosis induced by detachment from the extracellular

CC matrix. The Akt-3 nucleic acid molecule and protein may be used as
CC medicaments for treating cancer. Agents which influence the activity of
CC Akt-3 protein, and so stimulate apoptosis, may also be used to treat
CC diseases associated with Akt-3
XX
SQ Sequence 479 AA;

Query Match 100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDPDLKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDPDLKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTCGTPGYLAPEVLEDND 180
Db 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTCGTPGYLAPEVLEDND 322

Qy 181 YGRAVDWGLGVVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 240
Db 323 YGRAVDWGLGVVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 382

Qy 241 KDPNKRILGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRILGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438

RESULT 9
AAU79420
ID AAU79420 standard; protein; 479 AA.
XX
AC AAU79420;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human protein kinase B gamma.
XX
KW Human; integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB;
KW gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotropic;
KW neuroprotective; cytosstatic; cancer.
XX
OS Homo sapiens.
XX
FN WO200222862-A2.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-GB004094.
XX
PR 12-SEP-2000; 2000GB-00022333.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Hiles ID, Ellis C;
XX
DR WPI; 2002-351896/38.
XX
PT Identifying agent that modulates interaction between integrin-linked
PT kinase and presenilin-1, useful for treating Alzheimer's disease, and
PT identifying agent that modulates protein kinase B or gamma secretase
PT activity.
XX
PS Disclosure; Page 50-52; 53pp; English.
XX
CC The invention relates to identifying an agent modulating interaction
CC between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising
CC providing ILK, PS1 or their functional variants, as first and second
CC components respectively, contacting the components in the presence of a

CC test agent under conditions that in absence of the agent, would permit
CC the components to interact and determining whether the agent is capable
CC of modulating the interaction between the components. Also included are
CC the method above where the components are protein kinase beta (PKB),
CC gamma secretase or their functional variants, test kits for carrying out
CC the methods and an agent identified by the methods. The methods are used
CC for identifying an agent that modulates interaction between ILK and PS1.
CC or PKB or gamma-secretase. The agent has therapeutic applications in
CC treating humans or animals, for treating a host suffering from a
CC condition associated with an interaction between ILK and PS1, activity of
CC PKB, activity of gamma-secretase, apoptosis, cancer and Alzheimer's
CC disease. The agent is also useful for manufacturing a medicament for use
CC in treatment of the above mentioned conditions. The present sequence
CC represents human protein kinase B gamma
XX
SQ Sequence 479 AA;

Query Match 100.0%; Score 1563; DB 5; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDPDLKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDPDLKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTCGTPGYLAPEVLEDND 180
Db 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTCGTPGYLAPEVLEDND 322

Qy 181 YGRAVDWGLGVVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 240
Db 323 YGRAVDWGLGVVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 382

Qy 241 KDPNKRILGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRILGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438

RESULT 10
ABB06998
ID ABB06998 standard; protein; 479 AA.
XX
AC ABB06998;
XX
DT 20-JUN-2002 (first entry)
XX
DE Human Akt3 protein SEQ ID NO:9.
XX
KW Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;
KW apoptosis; serine/threonine kinase; heat shock protein; anticancer;
KW cytosstatic; cardiant; vasotropic; hepatotropic; neuroprotective;
KW antidiabetic; neurotropic; cancer; diabetes; Alzheimer's disease;
KW cell death; radiation; brain ischaemia; cardiac ischaemia.
XX
OS Homo sapiens.
XX
FN WO200215925-A1.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-JP007179.
XX
PR 22-AUG-2000; 2000JP-00251529.
XX
PA (KYOWA) KYOWA HAKKO KOGYO KK.
PA (TSUR/) TSURUO T.
XX
PI Tsuruo T, Fujita N, Sato S;
XX

DR WPI: 2002-292035/33.
 XX N-PSDB; ABL50839.
 PT Regulation of apoptosis by promoting or inhibiting the intracellular
 PT binding of Akt with Hsp90, useful for prevention and treatment of
 PT apoptosis-regulation associated diseases including cancer.
 XX
 PS Claim 12; Page 85-87; 93pp; Japanese.
 XX
 CC The present invention describes the regulation of apoptosis, in which the
 CC intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a
 CC heat-shock protein) is promoted or inhibited. The present invention also
 CC describes: (1) isoforms of Akt and Hsp90, and their partial peptides
 CC including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA
 CC encoding Akt or Hsp90 or their partial peptides including the binding
 CC domain; (4) expression vectors containing the DNA; (5) host cells
 CC transformed by the vectors; (6) production of Akt or Hsp90 or their
 CC partial peptides including the binding domain by culture of the
 CC transformed cells; (7) screening compounds for their ability to modify
 CC intracellular Akt activity by contact with cells expressing Akt or Hsp90;
 CC and (8) drug compositions containing antibodies recognizing the binding
 CC domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and
 CC Hsp90 have cytostatic, cardiant, vasotropic, hepatotropic, antidiabetic,
 CC neuroprotective and neurotropic activities. Blockade of the binding of
 CC Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.
 CC Akt and Hsp90 can be used in the prevention and treatment of diseases
 CC with which apoptosis regulation is associated, including cancer (such as
 CC gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and
 CC prostate cancer), diabetes, Alzheimer's disease, cell death caused by
 CC radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The
 CC present sequence represents human Akt3 which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 479 AA;
 Query Match 100.0%; Score 1563; DB 5; Length 479;
 Best Local Similarity 100.0%; Pred. No. 1.2e-155;
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60
 DB 143 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202
 QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 120
 DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 262
 QY 121 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
 DB 263 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 322
 QY 181 YGRAVDWGLGVVYEMMCGRLPFYVNDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
 DB 323 YGRAVDWGLGVVYEMMCGRLPFYVNDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
 QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
 DB 383 KDPNKRLLGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPFPKQVTSSETDTRYFDEE 438
 RESULT 11
 ABR57474
 ID ABR57474 standard; protein; 479 AA.
 XX
 AC ABR57474;
 XX
 DT 15-SEP-2003 (first entry)
 DE Human PKB-gamma amino acid sequence.
 XX
 KW Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;
 KW protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;
 KW neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;

KW structural analysis; cancer; diabetes; erectile dysfunction; human;
 KW neurodegeneration.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016516-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-GB003735.
 XX
 PR 14-AUG-2001; 2001GB-00019860.
 PR 01-MAY-2002; 2002GB-00009985.
 XX
 XX (NOVS) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.
 PA (CANC-) CANCER RES INST.
 XX
 PI Barford D, Yang J, Hemmings BA, Cron PD;
 XX WPI: 2003-268328/26.
 DR
 XX New crystal of protein kinase B beta, useful for activating protein
 PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates
 PT or a tetragonal space group.
 XX
 PS Disclosure; Fig 7; 284pp; English.
 XX
 CC The present invention describes a crystal of protein kinase B beta
 CC (PKBbeta) comprising (i), where (i) comprises: (a) a tetragonal space
 CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus
 CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or
 CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40
 CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =
 CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,
 CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5
 CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus
 CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in
 CC the specification. (i) has cytostatic, antidiabetic, vasotropic,
 CC neurotropic and neuroprotective activities, and can be used in gene
 CC therapy. The crystal of PKBbeta, and methods from the present invention,
 CC are useful in activating protein kinases, particularly AGC kinases, for
 CC identifying modulators of protein kinase activity, and for structural
 CC analysis of other protein kinases. The crystal may also be used in
 CC manufacturing a medicament for treating cancers, diabetes, erectile
 CC dysfunction or neurodegeneration. The present sequence represents the
 CC human PKB-gamma amino acid sequence, which is given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 479 AA;
 Query Match 100.0%; Score 1563; DB 6; Length 479;
 Best Local Similarity 100.0%; Pred. No. 1.2e-155;
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60
 DB 143 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202
 QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 120
 DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 262
 QY 121 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
 DB 263 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 322
 QY 181 YGRAVDWGLGVVYEMMCGRLPFYVNDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
 DB 323 YGRAVDWGLGVVYEMMCGRLPFYVNDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
 QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
 DB 383 KDPNKRLLGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 12
ADF45034
ID ADF45034 standard; protein; 479 AA.
XX
AC ADF45034;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human kinase AKT3.
XX
KW Human; protein kinase; enzyme; inhibitor; AKT3.
XX
OS Homo sapiens.
XX
PN WO2003081210-A2.
XX
PD 02-OCT-2003.
XX
PF 20-MAR-2003; 2003WO-US008725.
XX
PR 21-MAR-2002; 2002US-0366892P.
XX
PA (SUNE-) SUNESIS PHARM INC.
XX
PI Prescott JC, Braisted A;
XX
DR WPI; 2003-865136/80.
XX
XX Identifying ligand binding to inactive conformation of target protein
PT kinase (T) comprises contacting the conformation modified (T) which
PT contains reactive group at binding site, with ligands and detecting
PT kinase-ligand conjugate formation.
XX
PS Disclosure; SEQ ID NO 3; 260pp; English.
XX
XX The present invention relates to a method for identifying a ligand (L),
CC which binds to an inactive conformation of target protein kinase (T). The
CC method involves contacting inactive conformation of (T), which contains
CC or is modified to contain a reactive group at or near a binding site of
CC interest, with one or more ligand candidates capable of covalently
CC bonding to the reactive group thus forming a kinase-(L) conjugate (C).
CC The method is useful for identifying protein kinase inhibitors that
CC preferentially bind to inactive conformation of a target protein kinase.
CC The present sequence is a protein kinase which may be modified via an
CC amino acid substitution, for use in the method of the invention.
XX
SQ Sequence 479 AA;
Query Match 100.0%; Score 1563; DB 7; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 202
Qy 61 TRHPFLSLKYSFQTKORLCFVMEYVNGGELFFHLSERVSEDRTPFYGAIVSALDYL 120
Db 203 TRHPFLSLKYSFQTKORLCFVMEYVNGGELFFHLSERVSEDRTPFYGAIVSALDYL 262
Qy 121 HSGKIVVRDLKLEMLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLEND 180
Db 263 HSGKIVVRDLKLEMLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLEND 322
Qy 181 YGRAVDWMLGVVMYEMMCCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240
Db 323 YGRAVDWMLGVVMYEMMCCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382
Qy 241 KDPNKRLLGGGDDAKEIMRHSFFSGVNWQDYVDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGDDAKEIMRHSFFSGVNWQDYVDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 13
ADN71940
ID ADN71940 standard; protein; 479 AA.
XX
AC ADN71940;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human serine/threonine kinase Akt-3 protein SEQ ID NO:26.
XX
KW kinase pathway inhibitor; anti-prostate cancer;
KW mitogen-activated protein kinase pathway inhibitor;
KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase pathway;
KW PI3K/Akt kinase pathway; cytosolic; MAP kinase inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
KW human; serine/threonine kinase Akt-3; chromosome 1.
XX
OS Homo sapiens.
XX
PN WO2004041185-A2.
XX
PD 21-MAY-2004.
XX
PF 31-OCT-2003; 2003WO-US034636.
XX
PR 31-OCT-2002; 2002US-0423340P.
XX
PA (UYRP) UNIV ROCHESTER.
XX
PI Chang C, Lee Y, Lin W;
XX
DR WPI; 2004-390508/36.
DR N-PSDB; ADN71939.
XX
XX Composition useful in the treatment of e.g. prostate cancer comprises a
PT kinase pathway inhibitor and an anti-prostate cancer compound.
XX
PS Disclosure; SEQ ID NO 26; 118pp; English.
XX
XX The present invention describes a composition (C1) which comprises a
CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
CC Also described: (1) identification of a mitogen-activated protein (MAP)
CC kinase pathway inhibitor involving incubating an antiandrogen or a
CC library of molecules with a cell containing an activable MAP kinase
CC pathway and selecting the molecules which inhibit the activation of the
CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
CC involving incubating a cell with hydroxyflutamide and potential
CC inhibitor, and assaying the level of activation of MAP kinase pathway or
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
CC cytosolic activity, and can be used as a MAP kinase inhibitor,
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
CC prostate cancer inhibitor; and for reducing the number of prostate cancer
CC cells in a sample. The composition C1 provides effective combination
CC therapy as compared to prior therapies. The present sequence represents
CC human serine/threonine kinase Akt-3, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 479 AA;
Query Match 100.0%; Score 1563; DB 8; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRRVFSRTRFYGAIVSALDYL 120
Db 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRRVFSRTRFYGAIVSALDYL 262
QY 121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
Db 263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 322
QY 181 YGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240
Db 323 YGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSRTRFYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSRTRFYFDEE 438
RESULT 14
ADQ88266
ID ADQ88266 standard; protein; 479 AA.
XX AC ADQ88266;
XX AC ADQ88266;
XX DT 21-OCT-2004 (first entry)
XX XX
DE Human 14180 protein, a rac gamma Ser/Thr protein kinase RAC-PK-gamma.
XX KW human; cardiovascular disorder; thrombotic disorder;
KW differential expression; gene therapy; aberrant vascularisation;
KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;
KW dyslipidaemia; high blood pressure; heart failure; cardiatic;
KW thrombolytic; anticoagulant; antilipemic; hypotensive; cardiatic;
KW rac gamma Ser/Thr protein kinase; RAC-PK-gamma; EC 2.7.1.-; enzyme.
XX OS Homo sapiens.
XX XX
PN WO2004063340-A2.
XX XX
PD 29-JUL-2004.
XX XX
PF 13-JAN-2004; 2004WO-US000393.
XX XX
PR 13-JAN-2003; 2003US-0439683P.
PR 05-FEB-2003; 2003US-0445216P.
PR 18-FEB-2003; 2003US-0448036P.
PR 12-MAR-2003; 2003US-0454189P.
PR 25-MAR-2003; 2003US-0457541P.
PR 29-APR-2003; 2003US-0466411P.
PR 08-MAY-2003; 2003US-0469041P.
PR 10-JUN-2003; 2003US-0477414P.
PR 13-JUN-2003; 2003US-0478560P.
PR 24-JUL-2003; 2003US-0489772P.
PR 28-JUL-2003; 2003US-0490660P.
PR 03-SEP-2003; 2003US-0499838P.
PR 22-SEP-2003; 2003US-0504786P.
PR 24-SEP-2003; 2003US-0505570P.
PR 17-OCT-2003; 2003US-0512418P.
PR 27-OCT-2003; 2003US-0514660P.
XX (MILL-) MILLENNIUM PHARM INC.
XX XX
XX Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;
PI Rogrigue-Way A, Tomlinson JE;
PI N-PSDB; ADQ88265.
XX XX
DR WPI; 2004-553729/53.
DR N-PSDB; ADQ88265.
XX XX
PT Identifying a compound for treating a cardiovascular or thrombotic
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
PT and detecting the binding.
XX XX
PS Claim 1; SEQ ID NO 108; 512pp; English.

XX This invention relates to a novel compound that is capable of treating a
CC cardiovascular or thrombotic disorder. Specifically, it refers to the
CC identification of nucleic acid molecules, and the encoded proteins
CC thereof, which are differentially expressed in cardiovascular disease
CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation.
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,
CC dyslipidaemia, high blood pressure or heart failure. As such, they
CC exhibit cardiant, thrombolytic, anticoagulant, antilipemic, hypotensive
CC and cardiant activities. This polypeptide sequence is a human protein
CC that is differentially expressed in a patient with a cardiovascular
CC disorder, given in an exemplification of the invention.
XX XX
SQ Sequence 479 AA;
Query Match 100.0%; Score 1563; DB 8; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTMNDFVLLKLGKGTGKVLVREKASGKYVAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFVLLKLGKGTGKVLVREKASGKYVAMKILKKEVIIAKDEVAHTLTESRVLKN 202
QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRRVFSRTRFYGAIVSALDYL 120
Db 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRRVFSRTRFYGAIVSALDYL 262
QY 121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
Db 263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 322
QY 181 YGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240
Db 323 YGRAVDWGLGVVMYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSRTRFYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSRTRFYFDEE 438
RESULT 15
AAG78021
ID AAG78021 standard; protein; 454 AA.
XX AC AAG78021;
XX AC AAG78021;
XX DT 31-JAN-2002 (first entry)
XX DE Akt3 related polypeptide.
XX XX
KW Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;
KW cerebrotrophic; neurotrophic; neuroprotective; antiarthritic;
KW osteopathic; vasotropic; hepatotrophic; inhibitor of apoptosis; ASK1;
KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;
KW ischaemia reperfusion injury; stroke; organ transplantation;
KW coronary artery bypass; tumour cell survival; gene therapy;
KW Alzheimer's disease; osteoarthritis.
XX OS Unidentified.
XX XX
PN WO200168850-A2.
XX XX
PD 20-SEP-2001.
XX XX
PF 09-MAR-2001; 2001WO-US007663.
XX XX
PR 14-MAR-2000; 2000US-00526043.

XX (AVET) AVENTIS PHARM PROD INC.
XX Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
XX WPI; 2001-582452/65.
XX
PT New nucleic acid encoding human Akt3 protein, useful for inhibiting cell
PT death and treating myocardial infarction, ischemia reperfusion injury
PT associated with stroke, liver damage and renal failure.
XX
XX Disclosure; Page 72-73; 73pp; English.
XX
XX The invention relates to human Akt3 protein (AH/PH-domain containing
CC serine/threonine kinase, Akt) comprising a fully defined sequence
CC (AAG78018) of 465 amino acids, its splice variant or allelic variant,
CC where the encoding polynucleotide hybridizes under stringent conditions
CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570
CC base pairs defined in the specification. Akt3 has cerebroprotective,
CC neurotrophic, neuroprotective, antiarthritic, osteopathic, vasotropic and
CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis
CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a
CC regulatory region is useful for inhibiting cell death in cardiac myocytes
CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial
CC infarction or ischemia reperfusion injury, particularly that associated
CC with stroke, liver damage, renal failure, organ transplantation or
CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving
CC Akt3 activity during treatment of patients suffering from myocardial
CC infarction or ischemia reperfusion injury and inhibitors of Akt3
CC activity decrease tumour cell survival and result in tumour regression.
CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the
CC quantity of cell death and final infarct size, resulting in improved post
CC -infarction function, improved quality of life and reduced mortality. In
CC patients with existing heart failure, gene therapy with Akt3 retards the
CC process of ventricular dilation and slows down disease progression. Akt3
CC gene therapy is useful for treating other disease states, involving cell
CC death by apoptosis, including Alzheimer's disease, liver degeneration or
CC osteoarthritis. Note: The present sequence is given in the sequence
CC listing but is not featured anywhere else in the specification
XX
SQ Sequence 454 AA;
Query Match 99.7%; Score 1558; DB 4; Length 454;
Best Local Similarity 99.7%; Pred. No. 3.6e-155;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202
Qy 61 TRHPFLTSLKYSFQTKORLCFVMEYVNGGELFFHLSRVPFSEDRTRFYGAEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKORLCFVMEYVNGGELFFHLSRVPFSEDRTRFYGAEIVSALDYL 262
Qy 121 HSGKIVYRDLKLENLMDKOGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEDND 180
Db 263 HSGKIVYRDLKLENLMDKOGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEDND 322
Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
Qy 241 KDPNKRLLGGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVTSFETDTRFYDDEE 296
Db 383 KDPNKRLLGGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVTSFETDTRFYDDEE 438

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OM protein - protein search, using sw model

Run on: February 13, 2006, 06:28:39 ; Search time 426 Seconds
(without alignments)
490.226 Million cell updates/sec

Title: US-10-601-311-1_COPY_143_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFKVV.....VPPFKPQVTSIDTRYDDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1563	100.0	465	2	Q5VTI2	HUMAN	Q5vti2 homo sapien
2	1563	100.0	466	2	Q56A86	HUMAN	Q56a86 homo sapien
3	1563	100.0	479	1	AKT3	HUMAN	Q9Y243 homo sapien
4	1563	100.0	479	1	AKT3	MOUSE	Q9Wua6 mus musculus
5	1563	100.0	479	2	Q5VTI1	HUMAN	Q5vti1 homo sapien
6	1563	100.0	479	2	Q6XW40	MOUSE	Q6xw40 mus musculus
7	1568	99.7	454	1	AKT3	RAT	Q63484 rattus norv
8	1428	91.4	523	2	Q4T057	TETNG	Q4t057 tetraodon n
9	1420.5	90.9	480	2	Q57513	CHICK	Q57513 gallus gall
10	1416.5	90.6	481	2	Q98TY9	XENLA	Q98ty9 xenopus lae
11	1402.5	89.7	480	2	Q5ER96	BOVIN	Q5er96 bos taurus
12	1396.5	89.3	1893	2	Q4RLN6	TETNG	Q4rln6 tetraodon n
13	1394.5	89.2	480	1	AKT1	RAT	Q4rln6 tetraodon n
14	1394.5	89.2	480	2	Q6GSA6	MOUSE	Q6gsa6 mus musculus
15	1394.5	89.2	501	1	AKT	MLVAT	P31748 akt8 murine
16	1394	89.2	479	2	Q8UUX0	BRARE	Q8uux0 brachydanio
17	1393.5	89.2	480	1	AKT1	HUMAN	P31749 homo sapien
18	1391.5	89.0	452	2	Q8BS26	MOUSE	Q8bs26 mus musculus
19	1391.5	89.0	480	1	AKT1	MOUSE	P31750 mus musculus
20	1391	89.0	353	2	Q8CE74	MOUSE	Q8ce74 mus musculus
21	1391	89.0	481	1	AKT2	HUMAN	P31751 homo sapien
22	1391	89.0	481	1	AKT2	MOUSE	Q60823 mus musculus
23	1389	88.9	486	2	Q72X15	XENLA	Q72x15 xenopus lae
24	1386	88.7	485	2	Q61P76	XENLA	Q61p76 xenopus lae
25	1383	88.5	419	2	Q519W5	CANFA	Q519w5 canis faml
26	1380	88.3	472	2	Q4SLA7	TETNG	Q4sla7 tetraodon n
27	1378.5	88.2	480	1	AKT1	BOVIN	Q01314 bos taurus
28	1378	88.2	478	2	Q802Y3	BRARE	Q802y3 brachydanio
29	1378	88.2	481	1	AKT2	RAT	P47197 rattus norv
30	1252	80.1	527	2	Q7QK56	ANOCA	Q7qk56 anopheles g
31	1249	79.9	486	2	Q95YJ0	ASTPE	Q95yj0 asterina pe

RESULT 1

ID	Q5VTI2_HUMAN	PRELIMINARY;	PRT;	465 AA.
AC	Q5VTI2;			
DT	01-FEB-2005 (Tremblrel. 29, Created)			
DT	01-FEB-2005 (Tremblrel. 29, Last sequence update)			
DT	13-SEP-2005 (Tremblrel. 31, Last annotation update)			
DE	V-akt murine thymoma viral oncogene homolog 3 (Protein kinase B, gamma).			
DE	gamma).			
GN	ORFNames=RP11-150L22.2-002;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Lad H.;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Wallis J.;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Howden P.;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
CC	- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.			
CC	- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
CC	- SIMILARITY: Contains 1 PH domain.			
DR	EMBL; AL592151; CAH72891.1; -; Genomic DNA.			
DR	EMBL; AL662889; CAH73072.1; -; Genomic DNA.			
DR	EMBL; AL591721; CAH71866.1; -; Genomic DNA.			
DR	EMBL; AC096539; CAH72891.1; JOINED; Genomic DNA.			
DR	EMBL; AL662889; CAH72891.1; JOINED; Genomic DNA.			
DR	EMBL; AL591721; CAH72891.1; JOINED; Genomic DNA.			
DR	EMBL; AL592151; CAH73072.1; JOINED; Genomic DNA.			
DR	EMBL; AL662889; CAH71866.1; JOINED; Genomic DNA.			
DR	EMBL; AC096539; CAH71866.1; JOINED; Genomic DNA.			
DR	EMBL; AL592151; CAH73072.1; JOINED; Genomic DNA.			
DR	EMBL; AC096539; CAH73072.1; JOINED; Genomic DNA.			
DR	SMR; QSVTI2; 1-115, 144-445.			
DR	Ensembl; ENSG00000117020; Homo sapiens.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR001849; PH.			
DR	InterPro; IPR001193; PH type.			
DR	InterPro; IPR000961; Pkinase C.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			

32	1248	79.8	528	2	Q868D7	AEDAE	Q868d7 aedes aegyp
33	1240	79.3	530	2	Q24293	DROME	Q24293 drosophila
34	1240	79.3	530	2	Q24469	DROME	Q24469 drosophila
35	1240	79.3	611	2	Q7JN11	DROME	Q7jnl1 drosophila
36	1240	79.3	611	2	Q8INB9	DROME	Q8inb9 drosophila
37	1233	78.9	591	2	Q4T3K9	TETNG	Q4t3k9 tetraodon n
38	1169	74.8	390	2	Q5I9W4	CANFA	Q5i9w4 canis faml
39	1118.5	71.6	546	2	Q17942	CAEEL	Q17942 caenorhabdi
40	1104	70.6	532	2	Q61K11	CAEEL	Q61k11 caenorhabdi
41	1098	70.2	541	2	Q17941	CAEEL	Q17941 caenorhabdi
42	1032	66.0	528	2	Q9XTG7	CAEEL	Q9xtg7 caenorhabdi
43	1027	65.7	483	2	Q77145	CAEEL	Q77145 caenorhabdi
44	983	62.9	387	2	Q8MUAS	HYDAT	Q8muas hydra atten
45	977	62.5	302	2	Q4TBD9	TETNG	Q4tbd9 tetraodon n

ALIGNMENTS

```
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 465 AA; 54032 MW; 592EF8B6937D1E0 CRC64;

Query Match 100.0%; Score 1563; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFYKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATNKTTCGTPPEYLAPVLEND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATNKTTCGTPPEYLAPVLEND 322

Qy 181 YGRAVDWGLGVVYEMWCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWGLGVVYEMWCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDPAKEIMRHSHFFSGVNWQDVYDKLVPPFPQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDPAKEIMRHSHFFSGVNWQDVYDKLVPPFPQVTSSETDTRYFDEE 438

RESULT 2
Q56A86 HUMAN PRELIMINARY; PRT; 466 AA.
ID Q56A86 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q56A86;
DC 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE AKT3 protein (Fragment).
GN Name=AKT3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RG NIH MSC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; BC020479; AAH20479.1; -; mRNA.
DR SMR; Q56A86; 1-115.
DR Ensembl; ENSG00000117020; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein-serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 466
SQ SEQUENCE 466 AA; 54288 MW; CE8576C2B48FCA6E CRC64;

Query Match 100.0%; Score 1563; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFYKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATNKTTCGTPPEYLAPVLEND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATNKTTCGTPPEYLAPVLEND 322

Qy 181 YGRAVDWGLGVVYEMWCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWGLGVVYEMWCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDPAKEIMRHSHFFSGVNWQDVYDKLVPPFPQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDPAKEIMRHSHFFSGVNWQDVYDKLVPPFPQVTSSETDTRYFDEE 438

RESULT 3
AKT3_HUMAN STANDARD; PRT; 479 AA.
ID AKT3_HUMAN
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AC Q9Y243; Q96QV3; Q9UFP5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
 DE (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (SFK-2).
 GN Name=AKT3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN NUCLEOTIDE SEQUENCE, AND MUTAGENESIS.
 RP MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;
 RA Brodbeck D., Cron P., Hemmings B.A.;
 RT "A human protein kinase B gamma with regulatory phosphorylation sites
 RT in the activation loop and in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 274:9133-9136(1999).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=99252329; PubMed=10208883; DOI=10.1006/bbrc.1999.0559;
 RA Nakatani K., Sakaue H., Thompson D.A., Weigel R.J., Roth R.A.;
 RT "Identification of a human Akt3 (protein kinase B gamma) which
 RT contains the regulatory serine phosphorylation site.";
 RL Biochem. Biophys. Res. Commun. 257:906-910(1999).
 RN [3]
 RN TISSUE=Brain;
 RP MEDLINE=99421751; PubMed=10491192;
 RA Masure S., Haefner B., Wesseling J.-J., Hoefnagel E., Mortier E.,
 RA Verhaselt P., Tuytelaars A., Gordon R., Richardson A.;
 RT "Molecular cloning, expression and characterization of the human
 RT serine/threonine kinase Akt-3.";
 RL Eur. J. Biochem. 265:353-360(1999).
 RN [4]
 RN NUCLEOTIDE SEQUENCE (ISOFORM 1).
 RP Li X., Yu L., Huang H., Zhang M., Zhao Y., Zhao S.;
 RT "Cloning of a novel human cDNA, STK-2, which encodes a rat serine-
 RT threonine protein kinase (STK) homolog.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).
 RP TISSUE=Testis;
 RA MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoef A., Beyer A., Koehrer K., Strack N.,
 RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 RN [6]
 RN NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), AND MUTAGENESIS OF THR-305 AND
 RP THR-447.
 RA Brodbeck D., Hill M.M., Hemmings B.A.;
 RT "Two splice variants of PKB gamma have different regulatory capacity
 RT depending on the presence or absence of the regulatory phosphorylation
 RT site Ser-472 in the C-terminal hydrophobic domain.";
 RL J. Biol. Chem. 276:29550-29558(2001).
 CC -!- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
 CC role in regulating cell survival. Capable of phosphorylating
 CC several known proteins. Truncated isoform 2/PKB gamma 1 without
 CC the second serine phosphorylation site could still be stimulated
 CC but to a lesser extent.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- INTERACTION:
 CC Q16543: CDC37; NbrExp=1; IntAct=EBI-296115, EBI-295634;
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
 CC cell stimulation leading to its translocation.
 CC -!- ALTERNATIVE PRODUCTS:
 CC

CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=PKB gamma;
 CC IsoId=Q9Y243-1; Sequence=Displayed;
 CC Name=2; Synonyms=PKB gamma 1;
 CC IsoId=Q9Y243-2; Sequence=VSP_004947;
 CC -!- TISSUE SPECIFICITY: In adult tissues, it is highly expressed in
 CC brain, lung and kidney, but weakly in heart, testis and liver. In
 CC fetal tissues, it is highly expressed in heart, liver and brain
 CC and not at all in kidney.
 CC -!- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
 CC kinase alpha (PI(3)K) results in its targeting to the plasma
 CC membrane.
 CC -!- PTM: Phosphorylated on threonine and serine residues.
 CC Phosphorylation on both serines and threonines is required for
 CC full activity.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 PH domain.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; AF124141; AAD29089.1; -; mRNA.
 DR EMBL; AF135794; AAD24196.1; -; mRNA.
 DR EMBL; AF085234; AAL40392.1; -; mRNA.
 DR EMBL; AJ245709; CAB53537.1; -; mRNA.
 DR EMBL; AL117525; CAB55977.1; ALT TERM; mRNA.
 DR EMBL; AY005799; AAF31073.1; -; mRNA.
 DR PIR; A59380; A59380.
 DR HSSP; P31751; IGZK.
 DR SMR; Q9Y243; 1-115.
 DR IntAct; Q9Y243; -.
 DR Ensembl; ENSG00000117020; Homo sapiens.
 DR HGNC; HGNC:393; AKT3.
 DR GO; GO:0004672; P:protein kinase activity; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011993; PH type.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKG; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
 KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 5 107 PH.
 FT NP_BIND 148 405 Protein kinase.
 FT ACT_SITE 271 271 ATP (By similarity).
 FT BINDING 177 177 ATP (By similarity).
 FT MOD_RES 305 305 Phosphothreonine (By similarity).
 FT MOD_RES 472 472 Phosphoserine (By similarity).
 FT VARSPPLIC 452 479 YDEGMDCMNERRRHPQFSASGRE -> CQSQDCGML
 FT GNWKK (in isoform 2).
 FT FTID-VSP_004947.
 FT T->A: No activation after pervanadate
 FT treatment.
 FT T->D: 2-fold increase of phosphorylation
 FT steady state level, no activation after
 FT

```
FT MUTAGEN 447 447 pervanadate treatment.
FT T->A: No effect.
FT MUTAGEN 447 447 T->D: No effect.
FT MUTAGEN 472 472 S->A: 67% decrease of activity after
FT pervanadate treatment.
FT MUTAGEN 472 472 S->D: 1.4-fold increase of
FT phosphorylation steady state level, 50%
FT decrease of activity after pervanadate
FT treatment.
SQ SEQUENCE 479 AA; 55775 MW; F08BDD6502E78FB CRC64;

Query Match 100.0%; Score 1563; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.9e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLEKLEMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 180
Db 263 HSGKIVYRDLEKLEMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 322

Qy 181 YGRAVDWVWGLGVVYEMVWCGRLPFYNQDHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMVWCGRLPFYNQDHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGDDAKEIMRHSFFSGVNVQDVYDKLVPPFPQVTSSETDTRFYDDE 296
Db 383 KDPNKRLLGGGDDAKEIMRHSFFSGVNVQDVYDKLVPPFPQVTSSETDTRFYDDE 438

RESULT 4
ID AKT3 MOUSE STANDARD; PRT; 479 AA.
AC Q9WUA6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
DE (Protein Kinase Akt-3) (Protein kinase B, gamma) (PKB gamma).
GN Name=Akt3;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;
RA Brodbeck D., Cron P., Hemmings B.A.;
RT "A human protein kinase B gamma with regulatory phosphorylation sites
RL in the activation loop and in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 274:9133-9136(1999).
RN [2]_
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX PubMed=11387345; DOI=10.1074/jbc.M104633200;
RA Brodbeck D., Hill M.M., Hemmings B.A.;
RT "Two splice variants of PKB gamma have different regulatory capacity
RT depending on the presence or absence of the regulatory phosphorylation
RT site Ser-472 in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 276:29550-29558(2001).
CC -!- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
CC role in regulating cell survival. Capable of phosphorylating
CC several known proteins. Truncated isoform 2/PKB gamma 1 without
CC the second serine phosphorylation site could still be stimulated
CC but to a lesser extent (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
```

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CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
CC cell stimulation leading to its translocation.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=PKB gamma;
CC IsoId=Q9WUA6-1; Sequence=Displayed;
CC Name=2; Synonyms=PKB gamma 1;
CC IsoId=Q9WUA6-2; Sequence=VSP_004948;
CC -!- TISSUE SPECIFICITY: Isoform 1 is expressed in prostate, testis,
CC uterus and mammary gland and isoform 2 is expressed in prostate,
CC testis and mammary gland.
CC -!- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -!- PTM: Phosphorylated on threonine and serine residues.
CC Phosphorylation on both sites is required for full activity.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF124142; AAD29090.1; -; mRNA.
CC HSP; P31751; IGZK.
CC SMR; Q9WUA6; 1-115.
CC DR Ensembl; ENSMUSG00000019699; Mus musculus.
CC MGI; MGI:1345147; Akt3.
CC DR InterPro; IPR001849; PH type.
CC DR InterPro; IPR011993; PH type.
CC DR InterPro; IPR000961; Kinase C.
CC DR InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR008271; Ser_thr_pkin_AS.
CC DR Pfam; PF00169; PH; 1.
CC DR Pfam; PF00069; Kinase; 1.
CC DR Pfam; PF00433; Kinase C; 1.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR PROSITE; PS00003; PH DOMAIN; 1.
CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
CC DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
CC Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 5 107 PH.
FT DOMAIN 148 405 Protein kinase.
FT NP_BIND 154 162 ATP (By similarity).
FT ACT_SITE 271 271 Proton acceptor (By similarity).
FT BINDING 177 177 ATP (By similarity).
FT MOD_RES 305 305 Phosphothreonine (By similarity).
FT MOD_RES 472 472 Phosphoserine (By similarity).
FT VARSP 452 479 YDDGDMGDMNRRPFPQFSYASGRE -> CQQSDCGML
FT /FTID=VSP_004948.
FT /FTID=VSP_004948.
SQ SEQUENCE 479 AA; 55714 MW; F08ACDF75743B8FB CRC64;

Query Match 100.0%; Score 1563; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.9e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLEKLEMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 180
Db 263 HSGKIVYRDLEKLEMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 322
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QY 181 YGRAVDWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
|||||
DB 323 YGRAVDWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
|||||
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
|||||
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 438
|||||

RESULT 5
QSVT11 HUMAN
ID QSVT11 HUMAN PRELIMINARY; PRT; 479 AA.
AC QSVT11
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE V-akt murine thymoma viral oncogene homolog 3 (Protein kinase B, gamma)
DE
GN ORFNames=RP11-150122.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lad H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wallis J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Howden P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein..
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -|- SIMILARITY: Contains 1 PH domain.
DR EMBL; AL592151; CAH72892.1; -; Genomic DNA.
DR EMBL; AL662889; CAH73073.1; -; Genomic DNA.
DR EMBL; AL591721; CAH72892.1; JOINED; Genomic DNA.
DR EMBL; AC096539; CAH72892.1; JOINED; Genomic DNA.
DR EMBL; AL662889; CAH72892.1; JOINED; Genomic DNA.
DR EMBL; AL591721; CAH72892.1; JOINED; Genomic DNA.
DR EMBL; AL591721; CAH73073.1; JOINED; Genomic DNA.
DR EMBL; AL592151; CAH71867.1; JOINED; Genomic DNA.
DR EMBL; AL662889; CAH71867.1; JOINED; Genomic DNA.
DR EMBL; AC096539; CAH71867.1; JOINED; Genomic DNA.
DR EMBL; AL592151; CAH73073.1; JOINED; Genomic DNA.
DR EMBL; AC096539; CAH73073.1; JOINED; Genomic DNA.
DR SMR; QSVT11; 1-115.
DR Ensembl; ENSG00000117020; Homo sapiens.
DR GO; GO:0005274; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR001993; PH type.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser thr pkin AS.
DR InterPro; IPR002290; Ser thr pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
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DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 479 AA; 55775 MW; F08BDD6502E78PB CRC64;

Query Match 100.0%; Score 1563; DB 2; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.9e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLLGKGTFGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVK 60
|||||
DB 143 KTMNDFYLLKLLGKGTFGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVK 202
|||||
QY 61 TRHPFLTSKYSFQTKRLCFVMYVNGGELFFHLSSRERVSSEDRTRYGAEIVSALDYL 120
|||||
DB 203 TRHPFLTSKYSFQTKRLCFVMYVNGGELFFHLSSRERVSSEDRTRYGAEIVSALDYL 262
|||||
QY 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPVLEND 180
|||||
DB 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPVLEND 322
|||||
QY 181 YGRAVDWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
|||||
DB 323 YGRAVDWGLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382
|||||
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296
|||||
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 438
|||||

RESULT 6
Q6NWX0 MOUSE
ID Q6NWX0 MOUSE PRELIMINARY; PRT; 479 AA.
AC Q6NWX0
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Thymoma viral proto-oncogene 3.
GN Name=Akt3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CD1; TISSUE=Neural Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bladesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CD1; TISSUE=Neural Stem Cell;
```

RA Director MGC Project;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; BC066861; AAH66861.1; -; mRNA.
 DR HSSP; P05132; 1APM.
 DR SMR; Q6NWX0; 1-115.
 DR Ensembl; ENSMUSG00000019699; Mus musculus.
 DR MGI; MGI:1345147; Akt3.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein-tyrosine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011993; PH type.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 479 AA; 55657 MW; FA31AC734651B92D CRC64;
 Query Match 100.0%; Score 1563; DB 2; Length 479;
 Best Local Similarity 100.0%; Pred. No. 8.9e-96;
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KTWNDFYKLLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 60
 Db 143 KTWNDFYKLLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 202
 Qy 61 TRHPLFLSLKYSFQTKORLCFVMEVNGGELFFHLSEKRVSEDRTRFYGABIVSALDYL 120
 Db 203 TRHPLFLSLKYSFQTKORLCFVMEVNGGELFFHLSEKRVSEDRTRFYGABIVSALDYL 262
 Qy 121 HSGKIVYRDLKLEMLDKDGHIKITDPLCKEGITDAATMKTFCGTPPYLAPVLENDND 180
 Db 263 HSGKIVYRDLKLEMLDKDGHIKITDPLCKEGITDAATMKTFCGTPPYLAPVLENDND 322
 Qy 181 YGRAVDWVGLGVVYEMWCGRLPFYNQDHEKLFELIMEDIKFPRTLSDDAKSLLSGLLI 240
 Db 323 YGRAVDWVGLGVVYEMWCGRLPFYNQDHEKLFELIMEDIKFPRTLSDDAKSLLSGLLI 382
 Qy 241 KDPNKRLLGGGDDAKEIMRHSFFSGVNWQDYDKLVPPPKPQVTSSETDTRYPDEE 296
 Db 383 KDPNKRLLGGGDDAKEIMRHSFFSGVNWQDYDKLVPPPKPQVTSSETDTRYPDEE 438
 RESULT 7
 AKT3_RAT
 ID - AKT3_RAT
 AC Q63484;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
 DE (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma).
 GN Name=Akt3;
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=96063640; PubMed=7489143;
 RA Konishi H., Kuroda S., Tanaka M., Matsuzaki H., Ono Y., Kameyama K.,
 HA Haga T., Kikawa U.,
 RT "Molecular cloning and characterization of a new member of the RAC
 RT protein kinase family: association of the pleckstrin homology domain
 RT of three types of RAC protein kinase with protein kinase C subtypes
 RT and beta gamma subunits of G proteins.";
 RL Biochem. Biophys. Res. Commun. 216:526-534(1995).
 CC -1- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
 CC role in regulating cell survival. Capable of phosphorylating
 CC several known proteins (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
 CC kinase alpha (PI(3)K) results in its targeting to the plasma
 CC membrane.
 CC -1- PMM: Phosphorylated on threonine and serine residues.
 CC Phosphorylation on both sites is required for full activity.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 PH domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; D49836; BAA08637.1; -; mRNA.
 DR PIR; JC4345; JC4345.
 DR HSSP; P31751; 1GZK.
 DR SMR; Q63484; 1-115, 144-445.
 DR GDI; G2390; Akt3.
 DR GO; GO:0005515; F:protein binding; IDA.
 DR GO; GO:0005080; F:protein kinase C binding; IDA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
 DR InterPro; IPR01849; PH.
 DR InterPro; IPR011993; PH type.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
 KW Serine/threonine-protein kinase; Transferase.
 FT DOMAIN 5 107 PH.
 FT DOMAIN 148 405 Protein kinase.
 FT NP BIND 154 162 ATP (By similarity).
 FT ACT SITE 271 271 Proton acceptor (By similarity).
 FT BINDING 177 177 ATP (By similarity).
 FT MOD RES 305 305 Phosphothreonine (By similarity).
 SQ SEQUENCE 454 AA; 52850 MW; 68072CF9DFEE876 CRC64;
 Query Match 99.7%; Score 1558; DB 1; Length 454;
 Best Local Similarity 99.7%; Pred. No. 1.8e-95;
 Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 KTWNDFYKLLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 60
 Db 143 KTWNDFYKLLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSIKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSEDTREYGAIVSALDYL 120
 Db 203 TRHPFLTSIKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSEDTREYGAIVSALDYL 262
 QY 121 HSGKIVYRDLEKLEMLDKDGHKITDGLCKEGITDAATMKTCGTPYLAPEVLEND 180
 Db 263 HSGKIVYRDLEKLEMLDKDGHKITDGLCKEGITDAATMKTCGTPYLAPEVLEND 322
 QY 181 YGRAVDWGLGVVYEMCMGRLPFFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
 Db 323 YGRAVDWGLGVVYEMCMGRLPFFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 382
 QY 241 KDPNKRLLGGPPDDAKELMRHSFSGVNMQDVYDKLVPPKPVQVTSDDTRYFDEE 296
 Db 383 KDPNKRLLGGPPDDAKELMRHSFSGVNMQDVYDKLVPPKPVQVTSDDTRYFDEE 438

RESULT 8
 QAT057_TETNG
 ID QAT057_TETNG PRELIMINARY; PRT; 523 AA.
 AC QAT057;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF11339, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG0009507001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaife D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poullain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
 FT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
 CC cycle. It is required in higher cells for entry into S-phase and
 CC mitosis. Component of the kinase complex that phosphorylates the
 CC repetitive C-terminus of RNA polymerase II. Catalytic component of
 CC MPF (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
 CC mature oocytes (By similarity).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -!- SIMILARITY: Contains 1 PH domain.
 DR EMBL; CAAB01011339; CAF93725.1; -; Genomic_DNA.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_Thr_pkin_AS.
 DR InterPro; IPR002290; Ser_Thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00133; S-TK_X; 1.
 DR SMART; SM00220; S-TK; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 FT NON TER 523
 SQ SEQUENCE 523 AA; 60242 MW; D2FC6BED3B92090F CRC64;
 Query Match 91.4%; Score 1428; DB 2; Length 523;
 Best Local Similarity 81.5%; Pred. No. 9.1e-87;
 Matches 277; Conservative 8; Mismatches 11; Indels 44; Gaps 2;
 QY 1 KTMNDFDYLKLLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHILTTSRVLKN 60
 Db 143 KTMNDFDYLKLLGKGTGKVLVREKASGTYAMKILKKEVIIAKDEVAHILTTSRVLKN 202
 QY 61 TRHPFLT-----SLKYSFQTKDRLCFVMEYVNGG----- 90
 Db 203 TRHPFLTVSTAWRRRRRGAGSDRCLSVCLQKRRKDRLCFVMEYVNGGVRAGGSVDLCA 262
 QY 91 -----LFFHLRSRVFSEDTREYGAIVSALDYLHSGKIVYRDLEKLEML 136
 Db 263 RGRCVTRVLSPPQLFFHLRSRVFSEDTREYGAIVSALDYLHSAKIVYRDLEKLEML 322
 QY 137 LDKDGHKITDGLCKEGITDAATMKTCGTPYLAPEVLENDYGRAVDWGLGVVME 196
 Db 323 LDKDGHKITDGLCKEGITDAATMKTCGTPYLAPEVLENDYGRGVDMWGLGVVME 382
 QY 197 MWCRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLIKDPNKRLLGGPPDDAKE 256
 Db 383 MWCRLPFYNQDHEKLFELILMEBIKFPRTLSSDAKSLGLLIKDPNKRLLGGPPDDAKE 442
 QY 257 IMRHSFSGVNMQDVYDKLVPPKPVQVTSDDTRYFDEE 296
 Db 443 IMRHSFSTIDQDLVDKLVPPKPVQVTSDDTRYFDEE 482

RESULT 9
 OS7513_CHICK
 ID OS7513_CHICK PRELIMINARY; PRT; 480 AA.
 AC OS7513;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Serine/threonine protein kinase.
 GN Name=akt1;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Theelen M., Swinkels S.U.M., de Jong M.D.M., Thomas A.A.M.,
 RA Verkleij A.J., Hanafusa H., Humbel B.,
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC EMBL; AF039943; AAB94767.1; -; mRNA.
 DR HSP; P31749; 1H10.
 DR SMR; OS7513; 3-121.
 DR Ensembl; ENSGALG00000011620; Gallus gallus.

DR GO:0005524; F:ATP binding; IEA.
 DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR011993; PH type.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00220; S_TK; 1.
 DR PROSITE: PS00003; PH DOMAIN; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 480 AA; 55724 MW; 3883447FD6689626 CRC64;

Query Match 90.9%; Score 1420.5; DB 2; Length 480;
 Best Local Similarity 89.5%; Pred. No. 2.6e-86;
 Matches 265; Conservative 18; Mismatches 12; Indels 1; Gaps 1;

QY 2 TMNDFYLLKLGKTFGKVIIVREKASGKYAMKILKEVIAKDEVAHTLTESRLVKNY 61
 DB 146 TMEFEYLLKLGKTFGKVIIVREKATGRYYAMKILKEVIAKDEVAHTLTENRVLQNS 205
 QY 62 RHPFLTSKYSFQTKDRLCFWMEYVNGGELFFHLSRERVSFSDTRFYGAIVSALDYHL 121
 DB 206 RHPFLTALKYSFQTHDRLCFWMEYANGGELFFHLSRERVSFSDRFRYGAIVSALDYHL 265
 QY 122 SGK-IVYRDLEKLEMLDKDGHKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEDND 180
 DB 266 SEKNVYRDLEKLEMLDKDGHKITDFGLCKEGIKDGMATKTCGTPPYLAPEVLEDND 325
 QY 181 YGRAVDWVGLGVVYEMMCGRLPFYNQDHEKLFELIMEDIKPRPTLSSDAKSLLSGLLI 240
 DB 326 YGRAVDWVGLGVVYEMMCGRLPFYNQDHEKLFELIMEDIKPRPTLSSDAKSLLSGLLK 385
 QY 241 KDPNKRLLGGGDDAKEIMRHSFFSGVNWQVYDKLVPPRPQVTSSETDTRYFDEE 296
 DB 386 KDPQRLLGGGDDAKEIMQHFFAGIVWQVYDKLVPPRPQVTSSETDTRYFDEE 441

RESULT 10
 Q98TV9_XENLA
 ID Q98TV9_XENLA PRELIMINARY; PRT; 481 AA.
 AC Q98TV9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Akt.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus; Xenopus.
 ON NCBI_TaxID=8355;
 RN NUCLEOTIDE SEQUENCE.
 RA Andersen C.B., Sakane H., Roth R.A., Conti M.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF317656; AAG59601.1; -; mRNA.
 DR HSSP; P31751; 1MRY.
 DR SMR; Q98TV9; 1-116.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001849; PH.

DR InterPro: IPR011993; PH type.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00169; PH; 1.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00233; PH; 1.
 DR SMART: SM00133; S_TK; 1.
 DR PROSITE: PS00003; PH DOMAIN; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 SQ SEQUENCE 481 AA; 56042 MW; FF56CFB9A6454303 CRC64;

Query Match 90.6%; Score 1416.5; DB 2; Length 481;
 Best Local Similarity 88.9%; Pred. No. 4.8e-86;
 Matches 263; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

QY 2 TMNDFYLLKLGKTFGKVIIVREKASGKYAMKILKEVIAKDEVAHTLTESRLVKNY 61
 DB 147 TMEFEYLLKLGKTFGKVIIVREKATGRYYAMKILKEVIAKDEVAHTLTENRVLQNS 206
 QY 62 RHPFLTSKYSFQTKDRLCFWMEYVNGGELFFHLSRERVSFSDTRFYGAIVSALDYHL 121
 DB 207 RHPFLTALKYSFQTHDRLCFWMEYANGGELFFHLSRERVSFSDRFRYGAIVSALDYHL 266
 QY 122 SGK-IVYRDLEKLEMLDKDGHKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEDND 180
 DB 267 SEKNVYRDLEKLEMLDKDGHKITDFGLCKEGIKDGMATKTCGTPPYLAPEVLEDND 326
 QY 181 YGRAVDWVGLGVVYEMMCGRLPFYNQDHEKLFELIMEDIKPRPTLSSDAKSLLSGLLI 240
 DB 327 YGRAVDWVGLGVVYEMMCGRLPFYNQDHEKLFELIMEDIKPRPTLSSDAKSLLSGLLK 386
 QY 241 KDPNKRLLGGGDDAKEIMRHSFFSGVNWQVYDKLVPPRPQVTSSETDTRYFDEE 296
 DB 387 KDPQRLLGGGDDAKEIMQHFFAGIVWQVYDKLVPPRPQVTSSETDTRYFDEE 442

RESULT 11
 Q5ER96_BOVIN
 ID Q5ER96_BOVIN PRELIMINARY; PRT; 480 AA.
 AC Q5ER96;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE V-akt murine thymoma viral oncogene-like protein 1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Khatib H.;
 RT "Complete sequence of the bovine AKT1 gene."
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AY781100; AA71957.1; -; mRNA.
 DR SMR; Q5ER96; 3-121.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000961; Pkinase_C.


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DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00003; PH DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 55748 MW; 152E6613C4E6ED5A CRC64;

Query Match      89.3%; Score 1402.5; DB 2; Length 480;
Best Local Similarity 88.5%; Pred. No. 4.1e-85;
Matches 262; Conservative 19; Mismatches 14; Indels 1; Gaps 1;

QY 2 TNNDPDKLLKGGTGGKGVILVREKASGKYVAMKILKEVIITAKDEVAHTLTESRLVNT 61
DB 146 TNNDPEYLLKLLGKGTGGKGVILVREKATGRYVAMKILKEVIIVAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYNGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 265

QY 122 SGK-IVYRDLKLENLMDKGGHKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
DB 266 SEKEVYVYRDLKLENLMDKGGHKITDFGLCKEGIKDGAATMTKTCGTPPYLAPEVLEND 325

QY 181 YGRAVDWNGLGVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 326 YGRAVDWNGLGVMYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLSPKASLGLLK 385

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKQVTSSETDTRFYFDEE 296
DB 386 KDPKRLGGSGSEDAKEIMQRRFPASIVQDVYKLVPPFKQVTSSETDTRFYFDEE 441

RESULT 12
Q4RLN6 TETNG
AC Q4RLN6;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Chromosome 10 SCARF15019, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0032408001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lufalla G., Dossat C., Segreus B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cottolico L., Poullain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Gulgo B., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (by similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 PH domain.
DR EMBL: CAAB01015019; CAG10696.1; -; Genomic_DNA.
DR InterPro: IPR000253; PHA.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00498; PHA; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00240; PHA; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00006; PH DOMAIN; 1.
DR PROSITE: PS00003; PH DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 1893
SQ SEQUENCE 1893 AA; 210868 MW; 7F9B5064C2BC2632 CRC64;

Query Match      89.3%; Score 1396.5; DB 2; Length 1893;
Best Local Similarity 87.2%; Pred. No. 4.6e-84;
Matches 258; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

QY 2 TNNDPDKLLKGGTGGKGVILVREKASGKYVAMKILKEVIITAKDEVAHTLTESRLVNT 61
DB 124 TNNDPEYLLKLLGKGTGGKGVILVREKATGRYVAMKILKEVIIVAKDEVAHTLTENRVLQNS 183

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYNGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 121
DB 184 RHPFLTGLKYSFQTHDRLCFVMEYANGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 243

QY 122 SGK-IVYRDLKLENLMDKGGHKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
DB 244 AERNVYVYRDLKLENLMDKGGHKITDFGLCKEGIKDGAATMTKTCGTPPYLAPEVLEND 303

QY 181 YGRAVDWNGLGVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240
DB 304 YGRAVDWNGLGVMYEMMCGRLPFYNQDHEKLFELILMEDIRFPRTLSPKASLGLLK 363

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKQVTSSETDTRFYFDEE 296
DB 386 KDPKRLGGSGSEDAKEIMQRRFPASIVQDVYKLVPPFKQVTSSETDTRFYFDEE 441

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Dd 364 KDPWRLGGGPDDAKEIMQHFFAGIEWKDYVEKLVPPFPKQVTSYDTRFYDDE 419

RESULT 13

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AKT1_RAT
ID AKT1_RAT STANDARD; PRT; 480 AA.
AC P47196;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE RAC-alpha serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-alpha)
DE (Protein kinase B) (PKB).
GN Name=Akt1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=95091823; PubMed=7999118;
RA Konishi H., Shinomura T., Kuroda S.I., Ono Y., Kikkawa U.;
RT "Molecular cloning of rat RAC protein kinase alpha and beta and their
RL Biochem. Biophys. Res. Commun. 205:817-825(1994).
CC -!- FUNCTION: General protein kinase capable of phosphorylating
CC several known proteins. Phosphorylates TBCLD4 (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear after activation by
CC integrin-linked protein kinase 1 (ILK1) (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed. Low levels found in liver
CC with slightly higher levels present in thymus and testis.
CC -!- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -!- PTM: Phosphorylation on Thr-308, Ser-473 and Tyr-474 is required
CC for full activity. Ser-473 is dephosphorylated by PHLPP (By
CC similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D30040; BAA06279.1; -; mRNA.
CC PIR; JC2437; JC2437.
CC HSSP; P31749; 1H10.
CC SRR; P47196; 3-121.
CC Ensembl; ENSRNOG00000028629; Rattus norvegicus.
CC RGD; 2081; Akt1.
CC GO; GO:0005515; F:protein binding; IDA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
CC GO; GO:0006916; P:anti-apoptosis; IMP.
CC GO; GO:0030307; P:positive regulation of cell growth; IDA.
CC GO; GO:0007185; P:signal transduction; IDA.
CC InterPro; IPR001849; PH.
CC InterPro; IPR011993; PH type.
CC InterPro; IPR000961; Pkinase.C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkinase.
CC Pfam; PF00169; PH; 1.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00233; PH; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKC; 1.
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DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 5 108 PH.
FT DOMAIN 150 408 Protein kinase.
FT NP_BIND 156 164 ATP (By similarity).
FT ACT_SITE 274 274 Proton acceptor (By similarity).
FT BINDING 179 179 ATP (By similarity).
FT MOD_RES 308 308 Phosphothreonine (by PDK1) (By
FT similarity).
FT MOD_RES 473 473 Phosphoserine (by ILK1) (By similarity).
FT MOD_RES 474 474 Phosphotyrosine (By similarity).
SQ SEQUENCE 480 AA; 55735 MW; 5DCAAE7134366D04 CRC64;
Query Match 89.2%; Score 1394.5; DB 1; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.4e-84;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;
Qy 2 TMNDPDLKLLGKGTGKVLVREKASGKYAMKILKEVIIAKDEVAHILTESVLKNT 61
Db 146 TMEFEYLKLLGKGTGKVLVREKATGRYAMKILKEVIKDEVAHILTESVLQNS 205
Qy 62 RHPLTSLKYSFOTKDLRCFVMEYVNGGELFFHLRSRVFSEDRTRFYGAIVSALDYH 121
Db 206 RHPLTALKYSFQTHDLRCFVMEYANGGELFFHLRSRVFSEDRTRFYGAIVSALDYH 265
Qy 122 SGK-IVYRDLEKLENMLDKDGHKITDGLCKEGITDAATMKTCGTPYLAPEVLEDND 180
Db 266 SEKNVYVYRDLEKLENMLDKDGHKITDGLCKEGIKDGMATKTCGTPYLAPEVLEDND 325
Qy 181 YGRAVDWVGLGVVYEMMCGRLPFYNQDHEKLELIMEDIKPRTLSSDAKSLLSGLLI 240
Db 326 YGRAVDWVGLGVVYEMMCGRLPFYNQDHEKLELIMEDIKPRTLSSDAKSLLSGLLK 385
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQVYDKLVPPFPKQVTSYDTRFYDDE 296
Db 386 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQVYDKLVPPFPKQVTSYDTRFYDDE 441
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RESULT 14

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O6GSA6_MOUSE
ID O6GSA6_MOUSE PRELIMINARY; PRT; 480 AA.
AC O6GSA6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Thymoma viral proto-oncogene 1 (protein kinase B-alpha).
GN Name=Akt1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RX MEDLINE=22803305; PubMed=12783884; DOI=10.1074/jbc.M302847200;
RA Yang Z.Z., Tschopp O., Hemmings-Mieszczak M., Feng J., Brodbeck D.,
RA Perentes E., Hemmings B.A.;
RT "Protein Kinase B(alpha)/Akt1 Regulates Placental Development and
RT Fetal Growth.";
RL J. Biol. Chem. 278:32124-32131 (2003).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvJ;
RA Yang Z., Hemmings B.A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 PH domain.
DR EMBL; AF534134; AAN04036.1; -; Genomic_DNA.
DR EMBL; BC066018; AAH66018.1; -; mRNA.
DR SMR; QGSGA6; 3-121.
DR Ensembl; ENSMUSG00000001729; Mus musculus.
DR MGI; MGI:87986; Akt1.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0030027; C:lamellipodium; IDA.
DR GO; GO:0005819; C:spindle; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004672; F:protein kinase activity; IDA.
DR GO; GO:0042640; P:anagen; IMP.
DR GO; GO:0006915; P:apoptosis; IDA.
DR GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.
DR GO; GO:0007281; P:germ cell development; IDA.
DR GO; GO:0043066; P:negative regulation of apoptosis; IDA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR GO; GO:0030163; P:protein catabolism; IDA.
DR GO; GO:0016567; P:protein ubiquitination; IDA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; transferase.
SQ SEQUENCE 480 AA; 55707 MW; 98DF28E5EFE03730 CRC64;

Query Match      89.2%; Score 1394.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 14e-84;
Matches 260; Conservative 20; Mismatches 15; Indels 1;

QY 2 TNANDPYLKLCKCTFGKVIIVREKASGYYAMKILKKEVIAKDEVAHTLTESRVKVT 61
DB 146 TMNEFEYLLKLGKGTFGKVIIVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205
QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVSFSDRTFRFYGAETVSALDYLLH 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVSFSDRARFYGAETVSALDYLLH 265
QY 122 SGK-IVYRDLKLENLMLDKOGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEDND 180
DB 266 SEKNVYRDLKLENLMLDKOGHIKITDFGLCKEGIKDGTATMTFCGTPPYLAPEVLEDND 325
QY 181 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEDIKFPRTLSDDAKSLSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYQNDHEKLFELILMEEIRFPRTLGEAKSLSLGLLK 385
QY 241 KDPNKRLLGGPDDAKEIMRHSPFSGVNVQDVYDKLVLPFPKQVTSSETDTRYPFDEE 296
DB 386 KDPTQRLGGSEDAKEIMQHRRFFAIVQDVYVEKKLSPFPKQVTSSETDTRIFDEE 441

RESULT 15
AKT_MLVAT
ID AKT_MLVAT STANDARD; PRT; 501 AA.
AC P31748;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE AKT kinase transforming protein (EC 2.7.1.-).
GN Name=V-AKT;
OS AKT8 murine leukemia virus.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Gammaretrovirus.
OX NCBI_TaxID=11790;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=92022574; PubMed=1833819;
RA Bellacosa A., Testa J.R., Staal S.P., Tsichlis P.N.;
RT "A retroviral oncogene, akt, encoding a serine-threonine kinase
RT containing an SH2-like region.";
RL Science 254:274-277 (1991).
CC -!- PTM: Autophosphorylated on threonine and serine residues.
CC -!- MISCELLANEOUS: This protein is synthesized as a Gag-Akt
polyprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
subfamily.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M80675; AAA42545.1; -; Genomic_DNA.
DR HSSP; P31749; 1H10.
DR SMR; P31748; 24-142.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD0000001; Prot_kinase; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50109; PROTEIN_KINASE_ST; 1.
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DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding; Oncogene; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 26 129 PH.
FT DOMAIN 171 429 Protein kinase.
FT NP_BIND 177 185 ATP (By similarity).
FT ACT_SITE 295 295 Proton acceptor (By similarity).
FT BINDING 200 200 ATP (By similarity).
FT MOD_RES 347 347 Phosphotyrosine (By similarity).
SQ SEQUENCE 501 AA; 57870 MW; 5AEFDE58CD42F773 CRC64;

Query Match 89.2%; Score 1394.5; DB 1; Length 501;
Best Local Similarity 87.8%; Pred. No. 1.5e-84;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TMNDFYKLLGKGTGKVIILVREKASGKYAMKILKKEVIAKDEVAHTLTESVLKNT 61
Db 167 TMNEFEYLLKLGKGTGKVIILVREKATGRYAMKILKKEVIAKDEVAHTLTENRVLQNS 226
Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTPFYGAIVSALDYLH 121
Db 227 RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVSEDRARFYGAIVSALDYLH 286
Qy 122 SGK-IVYRDLKLENMLDKGHIKITDFGLCKEGITDAATMKTCGTPPYLAPEVLEDND 180
Db 287 SEKNVYRDLKLENMLDKGHIKITDFGLCKEGIKDGTWKTCGTPPYLAPEVLEDND 346
Qy 181 YGRAVDWGLGVVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEYV 240
Db 347 YGRAVDWGLGVVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEYVMEY 406
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296
Db 407 KDPTQRLGGGSEDAKEIMQHRFFANIVWQDVYVKKLSPPFPKQVTSSTDTRYFDEE 462

Search completed: February 13, 2006, 06:40:49
Job time : 429 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 06:33:54 ; Search time 73 Seconds
(without alignments)
390.139 Million cell updates/sec

Title: US-10-601-311-1_COPY_143_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFGKV.....VPPFKPQVSTDTRYFDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563	100.0	462	1 T17287	protein kinase (EC
2	1563	100.0	479	1 A59380	protein kinase (EC
3	1558	99.7	454	1 JC4345	protein kinase (EC
4	1394.5	89.2	480	1 JC2437	protein kinase (EC
5	1394.5	89.2	480	1 S33364	protein kinase (EC
6	1394.5	89.2	763	1 A40831	gag-akt polyprotei
7	1393.5	89.2	480	1 A39360	protein kinase (EC
8	1391	89.0	481	1 A46288	protein kinase (EC
9	1378.5	88.2	480	1 S62117	protein kinase (EC
10	1378	88.2	481	1 JC2438	protein kinase (EC
11	1240	79.3	611	1 A55888	protein kinase (EC
12	1118.5	71.6	546	1 T43233	protein kinase (EC
13	1098	70.2	541	1 T43232	protein kinase (EC
14	1032	66.0	528	1 T21523	protein kinase (EC
15	1027	65.7	483	1 T43234	protein kinase (EC
16	857	54.8	431	2 A48094	serum and glucocor
17	826	52.8	683	1 A23690	protein kinase (EC
18	822	52.6	683	1 S29478	protein kinase C (
19	819.5	52.4	736	1 KIRBCE	protein kinase C (
20	819.5	52.4	737	1 KINSC2	protein kinase C (
21	819.5	52.4	737	1 S28942	protein kinase C (
22	819	52.4	1016	1 A46079	protein kinase C (
23	815	52.1	682	1 A39666	protein kinase C (
24	811.5	51.9	737	1 KIRTC2	protein kinase C (
25	811	51.9	1096	1 S61917	protein kinase C (
26	807	51.6	1174	2 T43051	protein kinase C (
27	802	51.3	988	1 S35362	protein kinase C (
28	800.5	51.2	547	2 T28856	hypothetical prote
29	799.5	51.2	671	1 KIHUC1	protein kinase C (

30	798	51.1	634	1 B32392	protein kinase C (
31	797.5	51.0	671	1 KIRBC1	protein kinase C (
32	797.5	51.0	707	1 A53530	protein kinase C (
33	796.5	51.0	671	1 KIRTC1	protein kinase C (
34	796	50.9	1139	1 S61918	protein kinase C (
35	793	50.7	1102	2 T28666	protein kinase C-r
36	782	50.0	680	2 S37955	protein kinase YPK
37	779	49.8	672	1 KIBOC	protein kinase C (
38	779	49.8	673	1 KIBOC2	protein kinase C (
39	779	49.8	673	1 KIHUC2	protein kinase C (
40	779	49.8	673	2 S11213	protein kinase C (
41	778	49.8	422	2 T26334	hypothetical prote
42	778	49.8	672	1 KIRBC	protein kinase C (
43	777.5	49.7	479	2 A38578	protein kinase 2 (
44	777	49.7	672	1 KIHUCA	protein kinase C (
45	777	49.7	672	1 KIMSCA	protein kinase C (

ALIGNMENTS

RESULT 1

T17287
protein kinase (EC 2.7.1.37) akt3 short splice form - human
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protei
C:Species: Homo sapiens (man)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: T17287
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18723
A:Accession: T17287
A:Molecule type: mRNA
A:Residues: 1-462 <POU>
A:Cross-references: UNIPARC:UPI000016AC77; EMBL:AL117525; GB:CAB55977; NID:95912043; PID:
A:Experimental source: adult testis; clone DKFZp434N0250
R:Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.J
J. Biol. Chem. 274, 21528-21532, 1999
A:Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and andrpgen
A:Reference number: A64199; PMID:10419456
A:Contents: annotation
C:Comment: This protein is increased in estrogen receptor-negative breast cancers and an
C:Genetics:
A:Gene: GDB:AKT3
A:Cross-references: GDB:9954867
A:Map position: lq44-lq44
C:Function:
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F:4-105/Domain: pleckstrin repeat homology <PLK>
F:146-405/Domain: protein kinase homology <KIN>
F:154-162/Region: protein kinase ATP-binding motif
F:177/Active site: Lys #status predicted

Query Match	100.0%;	Score 1563;	DB 1;	Length 462;
Best Local Similarity	100.0%;	Pred. No. 1e-63;		
Matches 296;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	KTMNDFYLLKLGKTFGKVILVREKASGKYAMKILKEVIAKDEVAAHTLTESVLKN	60	
Db	143	KTMNDFYLLKLGKTFGKVILVREKASGKYAMKILKEVIAKDEVAAHTLTESVLKN	202	
QY	61	TRHPFLTSLKYSFQTKDRLCFVWEYVNGGELFPFHLSSRVFSEDTRFYGAEIVSALDYL	120	
Db	203	TRHPFLTSLKYSFQTKDRLCFVWEYVNGGELFPFHLSSRVFSEDTRFYGAEIVSALDYL	262	
QY	121	HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCFOTPRYLAPEVLDDND	180	
Db	263	HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCFOTPRYLAPEVLDDND	322	
QY	181	YGRANDWNGLVGVVYEMMCGRLPFFYNQDHEKLFELILMEDIKFPPTLSSDAKSLLSGLLI	240	

Db 323 YGRAVDWMGLGVVYEMVYKGLPFYVQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382
Qy 241 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 438
RESULT 2
A59380
protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human
N:Alternate names: protein kinase B gamma; RAC-pK-gamma; serine/threonine-specific protei
C:Species: Homo sapiens (man)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: A59380; MUID:99194749; PMID:10092583
R:Brodebeck, D.; Cron, P.; Hammings, B.A.
J. Biol. Chem. 274, 9133-9136, 1999
A:Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti
A:Reference number: A59380; MUID:99194749; PMID:10092583
A:Accession: A59380
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <BRO>
A:Cross-references: UNIPROT:Q9V243; UNIPARC:UPI00000335E8; GB:AD29089; NID:94757579; P
R:Maure, S.; Haetner, B.; Wesseling, J.J.; Hoefnagel, E.; Mortier, E.; Verhaaselt, P.;
Eur. J. Biochem. 265, 353-360, 1999
A:Title: Molecular cloning, expression and characterization of the human serine/threonin
A:Reference number: A59379; MUID:99421751; PMID:10491192
A:Accession: A59379
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-479 <MAS>
A:Cross-references: UNIPARC:UPI00000335E8; GB:CAB53537; NID:95804886; PIDN:CAB53537.1
C:Genetics:
A:Gene: GDB:AKT3; PKBG; PRK3G; RAC-gamma
A:Cross-references: GDB:9954867
A:Map position: lq44-lq44
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:7-108/Domain: pleckstrin repeat homology <PLK>
F:149-408/Domain: protein kinase homology <PK>
F:157-165/Region: protein kinase ATP-binding motif
F:177/Active site: Lys #status predicted
F:305/Binding site: phosphate (Thr) (covalent) #status predicted
F:474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte
Query Match 100.0%; Score 1563; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.le-63;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAEIVSALDYL 262
Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATWKTTCGTPPEYLAPEVLEND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATWKTTCGTPPEYLAPEVLEND 322
Qy 181 YGRAVDWMGLGVVYEMVYKGLPFYVQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWMGLGVVYEMVYKGLPFYVQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382
Query Match 100.0%; Score 1563; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.le-63;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAEIVSALDYL 262
Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATWKTTCGTPPEYLAPEVLEND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATWKTTCGTPPEYLAPEVLEND 322
Qy 181 YGRAVDWMGLGVVYEMVYKGLPFYVQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWMGLGVVYEMVYKGLPFYVQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382
Qy 241 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 438

RESULT 3
JC4345
protein kinase (EC 2.7.1.37) akt3 [validated] - rat
N:Alternate names: protein kinase B gamma; RAC-pK-gamma; serine/threonine-specific protei
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: JC4345
R:Konishi, H.; Kuroda, S.; Tanaka, M.; Mateuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; Ki
Biochem. Biophys. Res. Commun. 216, 526-534, 1995
A:Title: Molecular cloning and characterization of a new member of the RAC protein kinase
e C subtypes and beta gamma subunits of G proteins.
A:Reference number: JC4345; MUID:96063640; PMID:7488143
A:Accession: JC4345
A:Molecule type: mRNA
A:Residues: 1-454 <KON>
A:Cross-references: UNIPROT:Q63484; UNIPARC:UPI0000012577F; DBBJ:D49836; NID:g1136777; PII
A:Experimental source: brain
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:4-105/Domain: pleckstrin repeat homology <PLK>
F:146-405/Domain: protein kinase homology <KIN>
F:154-162/Region: protein kinase ATP-binding motif
F:177/Active site: Lys #status predicted
Query Match 99.7%; Score 1558; DB 1; Length 454;
Best Local Similarity 99.7%; Pred. No. 1.7e-63;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAEIVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAEIVSALDYL 262
Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATWKTTCGTPPEYLAPEVLEND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATWKTTCGTPPEYLAPEVLEND 322
Qy 181 YGRAVDWMGLGVVYEMVYKGLPFYVQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWMGLGVVYEMVYKGLPFYVQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382
Qy 241 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 438
RESULT 4
JC2437
protein kinase (EC 2.7.1.37) akt1 [validated] - rat
N:Alternate names: protein kinase B alpha; RAC-pK-alpha; serine/threonine-specific protei
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: JC2437
R:Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A:Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association
A:Reference number: JC2437; MUID:95091823; PMID:7999118
A:Accession: JC2437
A:Molecule type: mRNA
A:Residues: 1-480 <KON>
A:Cross-references: UNIPROT:P47196; UNIPARC:UPI0000012E044; DBBJ:D30040; NID:g485402; PDI
A:Experimental source: testis
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 89.2%; Score 1394.5; DB 1; Length 480;
Best Local Similarity 87.8%; Pred. No. 3.8e-56;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TWNDFDYLKLGKGFVKVILVREKASGYAMKILKKEVIIAKDEVAHTLTESRLVKN 61
Db 146 TNEFEYLLKLGKGFVKVILVREKATGRYAMKILKKEVIIVAKDEVAHTLTENRVLQNS 205

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 121
Db 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERFVSEDTRARFYGAETVSALDYH 265

Qy 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEND 180
Db 266 SEKNNVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGAATMKTFCGTPEYLAPEVLEND 325

Qy 191 YGRAVDWGLGVVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 240
Db 326 YGRAVDWGLGVVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 385

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 386 KDPTORLGGSEDAKEIMQHRFFANIVWQDVYEKKLSPFPKQVTSSETDTRYFDEE 441

RESULT 5

S33364
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: S33364
R;Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner, J
Oncogene 8, 745-754, 1993
A;Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt a
A;Reference number: S33364; PMID:93173519; PMID:8437858
A;Status: preliminary
A;Accession: S33364
A;Molecule type: mRNA
A;Residues: 1-480 <BEL>
A;Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID
C;Genetics:
A;Gene: MGI:Akt
A;Cross-references: MGI:87986
A;Map position: 12
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 89.2%; Score 1394.5; DB 1; Length 480;
Best Local Similarity 87.8%; Pred. No. 3.8e-56;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TWNDFDYLKLGKGFVKVILVREKASGYAMKILKKEVIIAKDEVAHTLTESRLVKN 61
Db 146 TNEFEYLLKLGKGFVKVILVREKATGRYAMKILKKEVIIVAKDEVAHTLTENRVLQNS 205

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 121
Db 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERFVSEDTRARFYGAETVSALDYH 265

Qy 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEND 180
Db 266 SEKNNVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGAATMKTFCGTPEYLAPEVLEND 325

Qy 191 YGRAVDWGLGVVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 240
Db 326 YGRAVDWGLGVVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 385

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 386 KDPTORLGGSEDAKEIMQHRFFANIVWQDVYEKKLSPFPKQVTSSETDTRYFDEE 441

RESULT 6

A40831
Gag-akt polyprotein - AKT8 murine leukemia virus
N;Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin
C;Species: AKT8 murine leukemia virus
C;Date: 12-Feb-1993 #sequence_revision 12-May-1994 #text_change 31-Dec-2004
C;Accession: A40831; B40831
R;Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.
Science 254, 274-277, 1991
A;Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH
A;Reference number: A40831; PMID:9202574; PMID:1833819
A;Accession: A40831
A;Molecule type: DNA
A;Residues: 1-262 <BEL>
A;Cross-references: UNIPARC:UPI000001725AF; GB:M80675
A;Accession: B40831
A;Molecule type: DNA
A;Residues: 262-763 <BE2>
A;Cross-references: UNIPARC:UPI000001725B0; GB:M80675
C;Genetics:
A;Gene: gag-akt
C;Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferase
F;1-129/Product: core protein p15 #status predicted <CP1>
F;130-214/Product: inner coat protein p12 #status predicted <CP2>
F;284-763/Product: kinase-related transforming protein akt #status predicted <AKT>
F;287-389/Domain: pleckstrin repeat homology <PLK>
F;431-691/Domain: protein kinase homology <KIN>
F;439-447/Region: protein kinase ATP-binding motif
F;25.337/Binding site: carboxylate (Asn) (covalent) #status predicted
F;462/Active site: Lys #status predicted
F;609/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 89.2%; Score 1394.5; DB 1; Length 763;
Best Local Similarity 87.8%; Pred. No. 5.5e-56;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TWNDFDYLKLGKGFVKVILVREKASGYAMKILKKEVIIAKDEVAHTLTESRLVKN 61
Db 429 TNEFEYLLKLGKGFVKVILVREKATGRYAMKILKKEVIIVAKDEVAHTLTENRVLQNS 488

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 121
Db 489 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERFVSEDTRARFYGAETVSALDYH 548

Qy 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEND 180
Db 549 SEKNNVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGAATMKTFCGTPEYLAPEVLEND 608

Qy 191 YGRAVDWGLGVVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 240
Db 609 YGRAVDWGLGVVMEYVNGGELFPHLSRERFVSEDTRFRFYGAETVSALDYH 668

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 669 KDPTORLGGSEDAKEIMQHRFFANIVWQDVYEKKLSPFPKQVTSSETDTRYFDEE 724

```
RESULT 7
A39360
protein kinase (EC 2.7.1.37) akt1 [validated] - human
N/Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C/Species: Homo sapiens (man)
C/Date: 20-Mar-1992 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C/Accession: A39360; S36389; S18000; S20836
R/Jones, P.F.; Jakubowicz, T.; Picossi, F.J.; Maurer, F.; Hemmings, B.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991
A/Title: Molecular cloning and identification of a serine/threonine protein kinase of th
A/Reference number: A39360; MUID:91239529; PMID:1851997
A/Accession: A39360
A/Molecule type: mRNA
A/Residues: 1-480 <JON>
A/Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E75B; GB:M63167; NID:g190827; PIDN:
R/Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A/Reference number: S24423; MUID:92249329; PMID:1533586
A/Contents: erratum
A/Accession: S36389
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, '
A/Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:g35480; PIDN:CAA43372.1; PID
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
A/Note: this a revision to the sequence from reference S17999
R/Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A/Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
A/Reference number: S17999; MUID:92037600; PMID:1718748
A/Accession: S18000
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 63-70, 'TPSSSAACGPISSNAPSWRLRLSGVDNRHPDCGRRPQ', 'EAGGGGDLPGVLTORQLRGRDRGGV
A/Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
A/Note: this sequence has been revised in reference S24423
R/Coffer, P.
submitted to the EMBL Data Library, July 1991
A/Reference number: S20836
A/Accession: S20836
A/Molecule type: mRNA
A/Residues: 63-70, 'TPSSSAACGPISSNAPSWRLRLSGVDNRHPDCGRRPQ', 'EAGGGGDLPGVLTORQLRGRDRGGV
A/Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037
A/Note: this sequence has been revised in reference S24423
R/Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming
EMBO J. 15, 6541-6551, 1996
A/Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
A/Reference number: A64192; MUID:97133284; PMID:8978681
A/Contents: annotation; phosphorylation sites
R/Toker, A.; Newton, A.C.
J. Biol. Chem. 275, 8271-8274, 2000
A/Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PL
A/Reference number: A64193; MUID:20187529; PMID:10722653
A/Contents: annotation; autophosphorylation site
C/Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidy-3
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.
C/Genetics:
A/Gene: GDB:AKT1; RAC; PKB
A/Cross-references: GDB:I18989; OMIM:164730
A/Map position: 14q32.32-14q32.32
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
e production
A/Pathway: signal transduction pathways regulating various processes including insulin a
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C/Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
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F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experimer

Query Match 89.2%; Score 1393.5; DB 1; Length 480;
Best Local Similarity 87.8%; Pred. No. 4.2e-56;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TMNDFDYLLKLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVKNT 61
DB 146 TMNEFEVYLKLLGKGTGKGVILVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRYFGAIVSALDYHL 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAIVSALDYHL 265

QY 122 SGK-IYVRDLKLENMLDKDGHKITDPLGCKEGITDAATMKTFCGTPEYLAPEVLEND 180
DB 266 SEKNVVRDLKLENMLDKDGHKITDPLGCKEGIKDGGATMKTFCGTPEYLAPEVLEND 325

QY 181 YGRAVDWMLGVVMEYEMMCGRLPFYVQDHEKLFELILMEDIKFPRTLTSSDAKSLLSGLLI 240
DB 326 YGRAVDWMLGVVMEYEMMCGRLPFYVQDHEKLFELILMEIRPRTLTGPEAKSLLSGLLK 385

QY 241 KDNKRLGGGPDDAKEIMRHSFSGVNMVDVYDKLVPPFPKQVTSQVTSQVTSQVTSQVTSQ 296
DB 386 KDPKQRLGGGSEDAKEIMQHRFFAGIYVQHVYKELSPFPKQVTSQVTSQVTSQVTSQVTSQ 441

RESULT 8
A46288
protein kinase (EC 2.7.1.37) akt2 - human
N/Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein
C/Species: Homo sapiens (man)
C/Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C/Accession: A46288
R/Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; Te
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992
A/Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/thr
A/Reference number: A46288; MUID:93028445; PMID:1409633
A/Accession: A46288
A/Molecule type: mRNA
A/Residues: 1-481 <CHE>
A/Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:g178325; PIDN:
A/Note: sequence extracted from NCBI backbone (NCBI:P:115859)
C/Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
C/Genetics:
A/Gene: GDB:AKT2
A/Cross-references: GDB:I135660; OMIM:164731
A/Map position: 19q13.2-19q13.2
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A/Pathway: signal transduction pathways regulating various processes
C/Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:150-409/Domain: protein kinase homology <KIN>
F:158-166/Region: protein kinase ATP-binding motif
F:181/Active site: Lys #status predicted

Query Match 89.0%; Score 1391; DB 1; Length 481;
Best Local Similarity 86.4%; Pred. No. 5.4e-56;
Matches 255; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

QY 2 TMNDFDYLLKLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVKNT 61
DB 148 TMNDFDYLLKLGKGTGKGVILVREKATGRYYAMKILKKEVIAKDEVAHTLTESRLVQNT 207

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRYFGAIVSALDYHL 121
DB 208 RHPFLTALKYAFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAIVSALEYHL 267

QY 122 SGKIVYRDLKLENMLDKDGHKITDPLGCKEGITDAATMKTFCGTPEYLAPEVLENDY 181
DB 268 SRDVIYRDLKLENMLDKDGHKITDPLGCKEGISDGGATMKTFCGTPEYLAPEVLENDY 327
```


Qy	182	GRAVDWGLGVVYVYEMMCGRLPFYFNQDHEKLPILMEDIKPPRTSSDAKSLLSGLLTK	241
Db	328	GRAVDWGLGVVYVYEMMCGRLPFYFNQDHERLPILMEEIRFPTLSPEAKSLAGLLKK	387
Qy	242	DPNKLGGGPPDDAKEMRHSFFSGVNWQDVYDKLVPPFKPQVTSFDTTRYFDEE	296
Db	388	DFKRLGGGSPDAKEWMEHRPFLSNWQDVQKLLPFEPKPOVTSFDTTRYFDEE	442

RESULT 9
 S62117
 protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
 N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Aug-2004
 C:Accession: S62117; S24423; S17999; S15714; S36388
 R:Coffer, P.J.; Woodgett, J.R.
 submitted to the EMBL Data Library, December 1991
 A:Reference number: S62117
 A:Accession: S62117
 A:Molecule type: mRNA
 A:Residues: 1-480 <COF>
 A:Cross-references: UNIPROT:Q01314; UNIPARC:UPI0000125042; EMBL:X61036; NID:g630; PIDN:C
 A:Note: this is a revision to the sequence from reference S17999
 R:Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 205, 1217, 1992
 A:Reference number: S24423; MUID:92249329; PMID:1533586
 A:Contents: erratum
 A:Accession: S24423
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 70-78,'N',80-145 <COW>
 A:Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036
 A:Note: this is a revision to the sequence from reference S17999
 R:Coffer, P.J.; Woodgett, J.R.
 Eur. J. Biochem. 201, 475-481, 1991
 A:Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
 A:Reference number: S17999; MUID:92037600; PMID:1718748
 A:Accession: S17999
 A:Molecule type: mRNA

Query Match 88.2%; Score 1378.5; DB 1; Length 480;
Best Local Similarity 87.2%; Pred. NO. 2e-55;
Matches 258; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

QY	2	TW	N	D	F	Y	L	K	L	G	K	G	T	F	G	K	V	I	L	R	E	K	S	G	K	Y	A	M	K	I	L	K	E	V	I	A	K	D	E	V	A	H	T	L	T	E	S	R	V	L	K	N	T	61	
Db	146	TN	N	E	F	Y	K	L	L	G	K	G	T	F	G	K	V	I	L	R	E	K	S	G	K	Y	A	M	K	I	L	K	E	V	I	A	K	D	E	V	A	H	T	L	T	E	N	R	V	L	K	N	205		
QY	62	RH	P	F	T	S	L	K	Y	S	F	Q	T	D	R	L	C	F	V	M	E	Y	N	G	G	B	E	L	F	H	L	S	R	E	R	V	F	S	D	R	T	F	Y	G	A	I	V	S	A	L	D	Y	L	H	121
Db	206	RH	P	S	T	A	L	K	Y	S	F	Q	T	D	R	L	C	F	V	M	E	Y	N	G	G	B	E	L	F	H	L	S	R	E	R	V	F	S	D	R	T	F	Y	G	A	I	V	S	A	L	D	Y	L	H	265
QY	122	SK	-	I	V	R	D	L	K	E	N	L	M	L	D	K	G	H	I	K	I	T	D	F	G	L	C	K	E	G	I	T	D	A	A	T	M	K	T	F	C	T	P	E	Y	L	A	P	E	V	I	D	N	180	
Db	266	SE	K	E	V	V	R	D	L	K	E	N	L	M	L	D	K	G	H	I	K	I	T	D	F	G	L	C	K	E	G	I	K	D	A	T	M	K	T	F	C	T	P	E	Y	L	A	P	E	V	I	D	N	325	
QY	181	YGR	A	D	V	M	G	L	G	V	V	Y	M	E	M	C	G	R	L	P	F	Y	N	Q	D	R	E	K	F	E	L	I	M	E	D	I	F	P	P	R	T	L	S	S	D	A	K	S	L	L	G	L	I	240	

Db	326	YGRAVDWMGLGVNVMCMGRLPFYQNQHEKLFELIMBEIRFPRTLSPEAKSLLSGLAK	385
Qy	241	KDPNKRILGGGDDAKEIMRHSFFSFGVNWQVDYDKLVPPFKQVMTSETTRPDEE	296
Db	386	KDPKRIKGGGSEDAKEIMHRRFFASIVQWDVYEKLSPPFKQVMTSETTRPDEE	441

RESULT 10
JC2438

Nucleotide sequence
Protein kinase (EC 2.7.1.37) akt2 [validated] - rat

N:Alternate names: protein kinase B beta; RAC-PK-Beta; serine/threonine-specific protein kinase B-beta; RSK-2; AKT2

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004

C:Accession: JG2438

F:Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 2005, 817-825, 1994

A>Title: Molecular cloning of rat RAC protein kinase alpha and beta and their association with phosphoinositide-dependent kinase-1.

A:Reference number: JC2437; MUID: 95091823; PMID: 7999118

R:A:Accession: JC2438

A:Molecule type: mRNA

A:Residues: 1-481 <CON>

A:Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577E; DDBJ:D330041; NID:G485404; PIDD:B330041

A:Experimental source: testis

C:Function:

D>Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate from ATP and peptide substrates containing Serine or Threonine residues

A:Pathway: signal transduction pathways regulating various processes including myoblast differentiation

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology, protein kinase C superfamily

C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase; pleckstrin repeat homology <PLK>
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:150-409/Domain: protein kinase domain <KIN>
F:158-166/Region: protein kinase ATR-binding motif
F:181/Active site: Lys #status predicted

Query Match 88.2%; Score 1378; DB 1; Length 481;

Best Local Similarity 85.8%; Pred. No. 2.1e-55;
Matches 253: Conservative 23: Mismatches 19: Indels 0: Gaps 0:

Qy 2 TMNDFYKLLGKGTFGKVILVREKASGKYAMKILKKEVI IANDEVAHTLTESVLKNT 61

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFVSEDTRFRFYGAIEIVSALDYH 121

QY	122	SGKIVVRLKLENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEDNDY	1811
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Qv	182	CPAVTWTGCGVAVVYEMMCCPIPEYVYVNDHKEFTPEIITLMEDIKEDPTTSSDAKSLISGIIITK	241
Db	268	STDVVYRIDIKLENMLDKDGHIKITDFGLSKEGISDGMTKTCGTPEYLAPEVLEDNDY	327

Db 328 GRAVDWGLGVVYEMMCGRLPFYQDHERLFELILMEEIRFPPTLGPESKSLLAGLKK 387

[illegible]

RESULT 11

A55888
protein kinase (EC 2.7.1.37) akt [similarity] - fruit fly (*Drosophila melanogaster*)
N;Alternate names: protein kinase B; RAC-PK; serine/threonine-specific protein kinase RAC
C;Species: *Drosophila melanogaster*
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A55888
J;Andjelkovic, M.; Jones, P.F.; Grossniklaus, U.; Cron, P.; Schier, A.F.; Dick, M.; Bilbe
J. Biol. Chem. 270, 4066-4075, 1995
A;Title: Developmental regulation of expression and activity of multiple forms of the Dr
A;Reference number: A55888; MUID:95181376; PMID:7876156
A;Accession: A55888
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-611 <AND>
A;Cross-references: UNIPROT:Q24469; UNIPARC:UPI00000866BE; GB:X83510
C;Genetics:
A;Gene: FlyBase:RacPK
A;Cross-references: FlyBase:FBgn0013324
A;Start codon: ACG
A;Introns: 261/3; 327/3; 457/3; 535/3; 584/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine
F;105-209/Domain: pleckstrin repeat homology <PLK>
F;264-523/Domain: protein kinase homology <KIN>
F;272-280/Region: protein kinase ATP-binding motif
F;295/Active site: Lys #status predicted
F;423/Binding site: phosphate (Thr) (covalent) #status predicted
F;586/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 79.3%; Score 1240; DB 1; Length 611;
Best Local Similarity 76.3%; Pred. No. 3.8e-49;
Matches 225; Conservative 35; Mismatches 35; Indels 0; Gaps 0;

Qy 2 TMNDFYLLKLGKTFGKVLVLRKASGKYVAMKILKEVIAKDEVAHTLTESRVLKNT 61
Db 262 TLENFEFLKVLGKTFGKVLCKREKATAKLYAIKILKEVIAKDEVAHTLTESRVLKST 321

Qy 62 RHPELTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSESDTRFYGAIEIVSALDYH 121
Db 322 NHPELTSLKYSFQNDRLCFVMEYVNGGELFFHLSHRIETEDTRFYGAIEIVSALGYLH 381

Qy 122 SGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLNDY 181
Db 382 SQGIYRDLEKLENMLDKDGHIKVADFGLCCKEDITYGRTYKTFCGTPEYLAPEVLNDY 441

Qy 182 GRAYDWMGLGVVYEMCGRLPFYVQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLIK 241
Db 442 GOAVDWMGTGVVYEMICGRLPFYVQDHEKLVFTLILVEVKFPRNITDEAKNLLAGLLAK 501

Qy 242 DPNKRLGGPDDAKEIMRHSFSGVNWQDVYDKLVPPPKPQVTSDDTRYFDEE 296
Db 502 DPKKRLGGKDDVKEIQAHPPFASINWTDLVLLKIPPPKQVTSDDTRYFDKE 556

RESULT 12
T43233
protein kinase (EC 2.7.1.37) akt-1 splice form b [similarity] - Caenorhabditis elegans
N;Alternate names: PKB; protein kinase B
C;Species: Caenorhabditis elegans
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: T43233; T19222
R;Paradis, S.; Ruvkun, G.
Genes Dev. 12, 2488-2498, 1998
A;Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AG
A;Reference number: Z22355; MUID:98382502; PMID:9716402
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-546 <PAR>
A;Cross-references: UNIPARC:UPI00000756DF; EMBL:AF072380; NID:g3694830;
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19092
A;Accession: T19222
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-546 <WIL>
A;Cross-references: UNIPARC:UPI00000756DF; EMBL:CAA98238.1; GSPDB:GN00023;
A;Experimental source: clone C12D8
C;Genetics:
A;Gene: akt-1; C12D8.10
A;Map position: 5
A;Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 323/3; 366/3; 487/3

C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating metabolism, development, and longevity
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
F;114-116/Domain: pleckstrin repeat homology <PLK>
F;191-455/Domain: protein kinase homology <KIN>
F;199-207/Region: protein kinase ATP-binding motif
F;222/Active site: Lys #status predicted
F;355/Binding site: phosphate (Thr) (covalent) #status predicted
F;522/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 71.6%; Score 1118.5; DB 1; Length 546;
Best Local Similarity 68.7%; Pred. No. 9.7e-44;
Matches 206; Conservative 40; Mismatches 49; Indels 5; Gaps 1;

Qy 2 TMNDFYLLKLGKTFGKVLVLRKASGKYVAMKILKEVIAKDEVAHTLTESRVLKNT 61
Db 189 TMEDFDKVLGKTFGKVLCKEKRTQKLYAIKILKDVIIAREVAHTLTENVLQRC 248

Qy 62 RHPELTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSR-----RVFSEDRTFYGAIEVSA 116
Db 249 KHPELTSLKYSFQNDRLCFVMEFAIGDLYYHLNRVQNMKEGFSRPRFYGEIVLA 308

Qy 117 LDYLHSGKIVYRDLEKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVL 176
Db 309 LGYLHANSIVYRDLEKLENMLDKDGHIKIADFGLCCKEISFGDKTSTFCGTPEYLAPEVL 368

Qy 177 EDDYGRADVWGLGVVYEMCGRLPFYVQDHEKLFELILMEDIKFPRTLSSDAKSLLS 236
Db 369 DDHYGRCDVWGVVYEMVCGRLPFYVQDHEKLFELIMAGDLRFPKLSQEAARTILT 428

Qy 237 GLLIKDNKRLGGPDDAKEIMRHSFSGVNWQDVYDKLVPPPKPQVTSDDTRYFDEE 296
Db 429 GLLVKDPTQRLGGPEDALEICRADFPRTVDWEATYRKEIEPPYKPNVQSEITDISYFDNE 488

RESULT 13
T43232
protein kinase (EC 2.7.1.37) akt-1 splice form a [similarity] - Caenorhabditis elegans
N;Alternate names: PKB; protein kinase B
C;Species: Caenorhabditis elegans
C;Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C;Accession: T43232; T19224
R;Paradis, S.; Ruvkun, G.
Genes Dev. 12, 2488-2498, 1998
A;Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AG
A;Reference number: Z22355; MUID:98382502; PMID:9716402
A;Accession: T43232
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-541 <PAR>
A;Cross-references: UNIPROT:Q17941; UNIPARC:UPI0000080469; EMBL:AF072379; NID:g3694828; I
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19092
A;Accession: T19224
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-541 <WIL>
A;Cross-references: UNIPARC:UPI0000080469; EMBL:Z73969; PIDN:CAA98240.1; GSPDB:GN00023; C
A;Experimental source: clone C12D8
C;Genetics:
A;Gene: akt-1; C12D8.10
A;Map position: 5
A;Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 318/3; 361/3; 482/3
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A;Pathway: signal transduction pathways regulating metabolism, development, and longevity
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
F;114-116/Domain: pleckstrin repeat homology <PLK>
F;191-450/Domain: protein kinase homology <KIN>

F:199-207/Region: protein kinase ATP-binding motif
F:222/Active site: Lys #status predicted
F:350/Binding site: phosphate (Thr) (covalent) #status predicted
F:517/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 70.2%; Score 1098; DB 1; Length 541;
Best Local Similarity 68.5%; Pred. No. 8e-43;
Matches 202; Conservative 39; Mismatches 54; Indels 0; Gaps 0;

QY 2 TMNDFYLLKLGKGTGKVLIVREKASGKYAMKILKEVIIIAKDEVAHVLTSRVLKNT 61
DB 189 TMEDFDLKLVLGKGTGKVLIVREKASGKYAMKILKEVIIIAKDEVAHVLTSRVLQRC 248
QY 62 RHPFLTSKYSPQKORLCFVMEYVNGELFFHLSRERVSFSDTRTFYGAIVSALDYHL 121
DB 249 KHPFLTELKYSFQHQYVLCFVMPANGELFTVHRKCGTSEPRARFYGAIVLALGYLH 308
QY 122 SGKIVYEDLKLNLMLDKDGHIKITDPLGCKEGITDAATMKTTCGTPYLAPVLEDNDY 181
DB 309 RCDIVYEDLKLNLMLDKDGHIKITDPLGCKEGITDAATMKTTCGTPYLAPVLEDNDY 368
QY 182 GRAYDWMGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLSGLLIK 241
DB 369 GRCVDWGVGVVYEMMCGRLPFYSKDNKLFELIMAGDLRFPFSKLSQEARITLTGLLYK 428
QY 242 DPNKRLGGGPDDAKEIMRHRSFFSGVNMQDYYDKLVPPFKPQVTSSETDTRYFDEE 296
DB 429 DPTQLRGSGPEDALEICRADFFRTVDWEATYKREIEPPYKPNVQSETDTSYFDNE 483

RESULT 14
T21523
protein kinase (EC 2.7.1.37) akt-2 long splice form [similarity] - Caenorhabditis elegans
N:Alternate names: PKB; protein kinase B
C:Species: Caenorhabditis elegans
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: T21523; T23878
R:McMurray, A.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z19434
A:Accession: T21523
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-528 <WtL>
A:Cross-references: UNIPROT:Q9XTG7; UNIPARC:UPI00000076045; EMBL:AL031621; PIDN:CAA20936
A:Experimental source: clone F28H6
R:McMurray, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19812
A:Accession: T23878
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-528 <Wt2>
A:Cross-references: UNIPARC:UPI00000076045; EMBL:Z92837; PIDN:CAB07403.1; GSPDB:GN000028;
A:Experimental source: clone R03E1
C:Genetics:
A:Gene: akt-2; CESP:F28H6.1
A:Map position: X
A:Introns: 32/2; 68/3; 135/3; 175/3; 241/3; 285/2; 305/3; 348/3; 459/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
A:Pathway: signal transduction pathways regulating metabolism, development, and longevity
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotransferase
F:111-113/Domain: pleckstrin repeat homology <PLK>
F:178-437/Domain: protein kinase homology <KIN>
F:186-194/Region: protein kinase ATP-binding motif
F:209/Active site: Lys #status predicted
F:337/Binding site: phosphate (Thr) (covalent) #status predicted
F:505/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 66.0%; Score 1032; DB 1; Length 528;
Best Local Similarity 65.8%; Pred. No. 7.1e-40;

Db 416 VPAKRLGAGPDDAREVSRAEFFKQVDWEATLRKEVEPPFKENNVNSETDTSEFFD 468

Search completed: February 13, 2006, 06:42:03
Job time : 74 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 05:32:58 ; Search time 197 Seconds
(without alignments)
8824.646 Million cell updates/sec

Title: US-10-601-311-2
Perfect score: 978
Sequence: 1 tctacaaccatcataaaag.....atggtatgactgatgcac 978

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/H COMB.seq.*
6: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	1547	3	US-09-851-670-1
2	949.8	97.1	1570	3	US-09-526-043-1
3	689	70.4	2410	3	US-09-771-161A-66
4	525	53.7	2626	3	US-09-590-740-5
5	515.8	52.7	1599	3	US-09-256-465-1
6	515.8	52.7	1599	3	US-09-167-322-3
7	515.8	52.7	1599	3	US-09-023-655-1004
8	510.6	52.2	2181	3	US-09-417-197-70
9	510.6	52.2	2184	3	US-09-417-197-138
10	510.6	52.2	2610	2	US-09-212-771-1
11	510.6	52.2	2610	3	US-09-091-058-1
12	510.6	52.2	2610	3	US-09-023-655-1206
13	510.6	52.2	2610	3	US-09-590-740-1
14	493	50.4	1254	3	US-09-590-740-3
15	383.8	39.2	387	3	US-09-474-922A-2
16	266.4	27.2	2239	3	US-09-949-016-1676
17	261.2	26.7	3255	3	US-09-016-434-1471
18	261.2	26.7	6102	3	US-09-949-016-2007
19	260.4	26.6	2370	3	US-09-031-295-1
20	260.4	26.6	2370	3	US-10-000-039-1
21	260.2	26.6	265	3	US-09-513-999C-2948
22	258.8	26.5	1338	3	US-10-067-977-1
23	257.6	26.3	2599	9	5266464-1
24	257.2	26.3	2311	2	US-08-712-709-6

25	257.2	26.3	2311	3	US-09-111-444-6	Sequence 6, Appli
26	257.2	26.3	2311	3	US-09-541-228-6	Sequence 6, Appli
27	257.2	26.3	2311	3	US-09-016-434-772	Sequence 772, App
28	255.8	26.2	2396	3	US-09-949-016-1735	Sequence 1735, Ap
29	246.4	25.2	3321	3	US-09-023-655-1361	Sequence 1361, Ap
30	240.4	24.6	2245	3	US-09-225-749-24	Sequence 24, Appli
31	239.4	24.5	2274	3	US-09-772-647-3	Sequence 3, Appli
32	239.4	24.5	2274	3	US-10-228-931-3	Sequence 3, Appli
33	238.6	24.0	532	3	US-09-270-767-14090	Sequence 14090, A
34	235.2	24.0	3456	3	US-09-487-558B-265	Sequence 265, App
35	233.2	23.8	2556	3	US-09-817-310-1	Sequence 1, Appli
36	233.2	23.8	2556	3	US-10-355-724A-1	Sequence 1, Appli
37	232	23.7	2244	3	US-09-094-714A-48	Sequence 48, Appli
38	229.8	23.5	1413	3	US-09-248-796A-4379	Sequence 4379, Ap
39	225.4	23.0	2127	3	US-09-270-767-13509	Sequence 13509, A
40	222.4	22.7	2346	3	US-09-762-258-3	Sequence 3, Appli
41	219.8	22.5	2751	3	US-09-417-197-72	Sequence 72, Appli
42	214.8	22.0	2324	3	US-09-190-976B-6	Sequence 6, Appli
43	213.6	21.8	2705	3	US-09-949-016-839	Sequence 839, App
44	213.6	21.8	2715	3	US-09-949-016-1959	Sequence 1959, Ap
45	212	21.7	2754	3	US-09-429-322-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-851-670-1
; Sequence: Application US/09851670
; Patent No. 6809194
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: AKT3 INHIBITORS
; FILE REFERENCE: PP-01699.002/200130.520
; CURRENT APPLICATION NUMBER: US/09/851,670
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-670-1

Query Match 100.0%; Score 978; DB 3; Length 1547;
Best Local Similarity 100.0%; Pred. No. 1.1e-267;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCTACAACCCATCATATAAAGAACATGAATGATTTTGTGACTATTTGAACTACTAGT	60
DB	416	TCTACAACCCATCATATAAAGAACATGAATGATTTTGTGACTATTTGAACTACTAGT	475
QY	61	AAAGGACATTTTGGGAAAGTATTTTGGTTCAGAGAGGCAAGTGGAAAACTATGCT	120
DB	476	AAAGGACATTTTGGGAAAGTATTTTGGTTCAGAGAGGCAAGTGGAAAACTATGCT	535
QY	121	ATGAAGATTCTCAAGAAAGAGTCAATTATTGCAAGAGATGAAGTGGCACACACTCTAACT	180
DB	536	ATGAAGATTCTCAAGAAAGAGTCAATTATTGCAAGAGATGAAGTGGCACACACTCTAACT	595
QY	181	GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTGAATAATTCCTTC	240
DB	596	GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTGAATAATTCCTTC	655
QY	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGGCGCTGTTTTC	300
DB	656	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGGCGCTGTTTTC	715
QY	301	CATTTGTGAGAGAGCGGGTGTCTCTGAGAGCCGACACACGTTTCTATCGTGCAGAAAT	360
DB	716	CATTTGTGAGAGAGCGGGTGTCTCTGAGAGCCGACACACGTTTCTATCGTGCAGAAAT	775

Qy 361 GTCTCTGCTTGGACTATCTATCATCTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db |||||
Qy 776 GTCTCTGCTTGGACTATCTATCATCTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 835
Db |||||
Qy 421 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGGACCTTGGCAAGAA 480
Db |||||
Qy 836 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGGACCTTGGCAAGAA 895
Db |||||
Qy 481 GGGATCAGATGCGAGCACCACATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 540
Db |||||
Qy 896 GGGATCAGATGCGAGCACCACATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 955
Db |||||
Qy 541 GAGGTGTTAGAATAATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db |||||
Qy 956 GAGGTGTTAGAATAATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015
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Qy 601 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACAGGACCATGAGAACTTTTT 660
Db |||||
Qy 1016 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACAGGACCATGAGAACTTTTT 1075
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Qy 661 GAATTAATATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db |||||
Qy 1076 GAATTAATATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1135
Db |||||
Qy 721 TTGCTTTTCAGGCTCTTTGATATAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 780
Db |||||
Qy 1136 TTGCTTTTCAGGCTCTTTGATATAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 1195
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Qy 781 GCAAAAGAAATTTATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 840
Db |||||
Qy 1196 GCAAAAGAAATTTATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 1255
Db |||||
Qy 841 AAAAAGCTTTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT 900
Db |||||
Qy 1256 AAAAAGCTTTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT 1315
Db |||||
Qy 901 GATGAAGAAATTTACAGCTCAGACTATTAACAATAACACCACTGAAAAATATGATGAGGAT 960
Db |||||
Qy 1316 GATGAAGAAATTTACAGCTCAGACTATTAACAATAACACCACTGAAAAATATGATGAGGAT 1375
Db |||||
Qy 961 GGTATGACTGCATGGAC 978
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Qy 1376 GGTATGACTGCATGGAC 1393
Db |||||

RESULT 2

US-09-526-043-1
; Sequence 1, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526.043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-09-526-043-1

Query Match 97.1%; Score 949.8; DB 3; Length 1570;
Best Local Similarity 99.8%; Pred. No. 1.2e-259;

Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TCTACAAACCCATCATATAAAGAAAGACAAATGAATGATTTTGGACTATTTGAAACTACTAGGT 60
Db |||||
Qy 531 TCTACAAACCCATCATATAAAGAAAGACAAATGAATGATTTTGGACTATTTGAAACTACTAGGT 590
Db |||||
Qy 61 AAAGGCACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 120
Db |||||
Qy 591 AAAGGCACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 650
Db |||||
Qy 121 ATGAAGATTTCTGAAGAAAGAAAGTCATTTATTTGCAAAAGGATGAAGTGGCACACACTCTAACT 180
Db |||||
Qy 651 ATGAAGATTTCTGAAGAAAGAAAGTCATTTATTTGCAAAAGGATGAAGTGGCACACACTCTAACT 710
Db |||||
Qy 181 GAAAGCAGAGTATTTAAAGAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTTCTTTC 240
Db |||||
Qy 711 GAAAGCAGAGTATTTAAAGAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTTCTTTC 770
Db |||||
Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300
Db |||||
Qy 771 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 830
Db |||||
Qy 301 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGGACACAGTTTCTATGTTGCAAAAT 360
Db |||||
Qy 831 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGGACACAGTTTCTATGTTGCAAAAT 890
Db |||||
Qy 361 GTCTCTGCTTGGACTATCTACATTTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db |||||
Qy 891 GTCTCTGCTTGGACTATCTACATTTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 950
Db |||||
Qy 421 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGGACTTTTGGCAAGAA 480
Db |||||
Qy 951 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGGACTTTTGGCAAGAA 1010
Db |||||
Qy 481 GGGATCAGATGCGAGCACCACATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 540
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Qy 1011 GGGATCAGATGCGAGCACCACATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 1070
Db |||||
Qy 541 GAGGTGTTAGAAGATTAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db |||||
Qy 1071 GAGGTGTTAGAAGATTAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1130
Db |||||
Qy 601 ATGTATGAATGATGTGTGGGAGGTTTACCTTTCTCAACACGAGGACCATGAGAACTTTTT 660
Db |||||
Qy 1131 ATGTATGAATGATGTGTGGGAGGTTTACCTTTCTCAACACGAGGACCATGAGAACTTTTT 1190
Db |||||
Qy 661 GAATTAATATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db |||||
Qy 1191 GAATTAATATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1250
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Qy 721 TTGCTTTTCAGGCTCTTTGATATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 780
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Qy 1251 TTGCTTTTCAGGCTCTTTGATATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 1310
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Qy 781 GCAAAAGAAATTTATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGATATGAT 840
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Qy 1311 GCAAAAGAAATTTATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGATATGAT 1370
Db |||||
Qy 841 AAAAGCTTGTACTCTCTTTTAAACCTCAAGTAACATCTCAGACAGATACCTAGATATTTT 900
Db |||||
Qy 1371 AAAAGCTTGTACTCTCTTTTAAACCTCAAGTAACATCTCAGACAGATACCTAGATATTTT 1430
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Qy 901 GATGAAGAAATTTACAGCTCAGACTATTTACAAATAACACCACTGAAAAATATGA 953
Db |||||
Qy 1431 GATGAAGAAATTTACAGCTCAGACTATTTACAAATAACACCACTGAAAAATATGA 1483
Db |||||

RESULT 3

US-09-771-161A-66
; Sequence 66, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.

; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 80620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 2410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-66

Query Match 70.4%; Score 689; DB 3; Length 2410;
Best Local Similarity 100.0%; Pred. No. 1.8e-185; Indels 0; Gaps 0;
Matches 689; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 290 AGCTGTTTTCATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACACGTTTCTATG 349
DB 312 AGCTGTTTTCATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATG 371
QY 350 GTGCAAAATTCCTCTGCTTGGACTATCTACATTCGGAAGAGATTGTACCGTGATC 409
DB 372 GTGCAAAATTCCTCTGCTTGGACTATCTACATTCGGAAGAGATTGTACCGTGATC 431
QY 410 TCAAGTTGGAGAACTTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGAC 469
DB 432 TCAAGTTGGAGAACTTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGAC 491
QY 470 TTTGCAAAAGAGGATCACAGATGAGCCACCATGAAGACATTTCTGTGSCACTCCAGAA 529
DB 492 TTTGCAAAAGAGGATCACAGATGAGCCACCATGAAGACATTTCTGTGSCACTCCAGAA 551
QY 530 APTCTGGACACAGAGGTGTAGAGATAATGACTATGGCCAGCAGTAGACTGGTGGGGCC 589
DB 552 ATCTGGACACAGAGGTGTAGAGATAATGACTATGGCCAGCAGTAGACTGGTGGGGCC 611
QY 590 TAGGGGTGTGATGAAATGATGTGGGAGGTACCTTTCTACAAACGAGGACCATG 649
DB 612 TAGGGGTGTGATGAAATGATGTGGGAGGTACCTTTCTACAAACGAGGACCATG 671
QY 650 AGAAACTTTTTCGAAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAG 709
DB 672 AGAAACTTTTTCGAAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAG 731
QY 710 ATGCAAAATTCATTTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGGAG 769
DB 732 ATGCAAAATTCATTTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGGAG 791
QY 770 GACCAAGATGATGCAAAAGAAATTAAGACACAGATTTCTTCTGTGAGTAAACTGGCAAG 829
DB 792 GACCAAGATGATGCAAAAGAAATTAAGACACAGATTTCTTCTGTGAGTAAACTGGCAAG 851
QY 830 ATGTATATGATAAAGCTGTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 889
DB 852 ATGTATATGATAAAGCTGTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 911
QY 890 CTAGATATTTTGTATGAAGAAATTAAGCTCAGACTATTACAAATAACACCACTGAAAT 949
DB 912 CTAGATATTTTGTATGAAGAAATTAAGCTCAGACTATTACAAATAACACCACTGAAAT 971
QY 950 ATGATGAGGATGGTATGGACTGATGGAC 978
DB 972 ATGATGAGGATGGTATGGACTGATGGAC 1000

RESULT 4
US-09-590-740-5

; Sequence 5, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-590-740-5

Query Match 53.7%; Score 525; DB 3; Length 2626;
Best Local Similarity 73.4%; Pred. No. 7.5e-139; Indels 3; Gaps 1;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;
QY 24 GACAAATGAATGATTTTGAATTAATTAAGTAAAGGACCTTTTGGGAAAGTTAT 83
DB 718 GACCAATGAACGATTTTGAATTAATTAAGTAAAGGACCTTTTGGGAAAGTTAT 777
QY 84 TTTGGTTTCGAGAGAGGCAAGTGGAAAAATATCTATGCTATGAAGATTTCTGAAGAAAGAT 143
DB 778 TCTGTTGAAAGAGAGAGGCAAGGCGGCTACTATGCCATGAAGATCCTCAAGAGAGGAT 837
QY 144 CATTAATGCAAGGATGAAGTGGCACACACTTAATTAAGTAAAGGACCTTTTAAAGAACAC 203
DB 838 CATGCTGCAAGGATGAGGTTGCCCAACGCTTACTGAGAACCGGTGCTCTGCAGAACTC 897
QY 204 TAGACATCCCTTTTAAACATCCTTCAAAATATTTCTTCCAGACAAAAGACCGTTTGTGTT 263
DB 898 TAGGATCCCTTCTTACGGCCCTCAAGTACTCATTCAGACCCAGACCGCCTCTGCTT 957
QY 264 TGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTCCATTTGTGAGAGAGCGGTGTT 323
DB 958 TGTGATGAGTATGCCAACGGGGGCGAGCTCTTCTTCCACTGTCTCGAGAGCGCGTGT 1017
QY 324 CTCTGAGACCGCACACGTTTCTATGTTGCGAATAATTTGCTCTGCTTGGACTATCTACA 383
DB 1018 CTCTGAGGACCGGGGCGGCTTCTATGTTGCGGAGATTTGTCTGCTGCTGCTGCTGCTG 1077
QY 384 TTCCGGGAAAGA---TTGTTGTTACCGTGATCTCAAGTTTGGAGAACTTAATCTCGACAAAGA 440
DB 1078 CTCCGAGAGAACGCTGTTGTTACCGGACCTGAACTGGAAGAACCTCATGCTCGACAAAGA 1137
QY 441 TGGCCACATATAAAATTAACAGATTTTGGACTTTTGAAGAGGAGGATCACAGATGCAAGCCAC 500
DB 1138 CGGGCACATCAAGATAACGGACTTCGGGCTGTGCAAGGAGGGGATCAAGGATGGTGGCCAC 1197
QY 501 CATGAAGACATCTCTGTCGACTCCAGATATCTGSCACAGAGGTGTTAGAAGATTAATGA 560
DB 1198 TATGAAGACATCTCTGCGAAACGCGGAGTACCTGGCCCTCTGAGGTGCTCGAGGACAAAGA 1257
QY 561 CTATCGCCGAGCAGTAGACTGTGGGGCTAGGGGTGTCATGATGAATGATGATGTTGTCG 620
DB 1258 CTACGGCCGTGAGTGGGACTGTGGGGGCTGGGGGCTGGGCTGATGATGATGATGTTG 1317
QY 621 GAGGTTTACCTTTCTTCAACACGAGGACCATGAGAAAATTTTGAATTAATTAATGAAGA 680
DB 1318 CGCCCTGCTTCTACACACGAGGACCAAGAGGCTGTTGAGAGTCTCTCATGGAGGA 1377
QY 681 CATTAATTTCTCGAAACACTCTCTTCAGATGCAAAATCATTTGCTTTAGGGCTCTTGAT 740
DB 1378 GATCGCTTCCCGGCACTCGGGCCCTGAGGCCAAGTCCCTGCTCTCGGGGCTGCTCAA 1437
QY 741 AAGGATCCAAATAAAGCGCTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGACA 800
DB 1438 GAAGGACCTTACACAGAGGCTCGTGGGGGCTCTGAGGATGCGCAAGGATCATGACGCA 1497

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Qy 801 CAGTTTCTTCTGTGAGTAACTGGCAAGATGTATATGATATAAAAGCTTGTACCTCTTT 860
Db 1498 CCGGTCTTTTCCCAACATCGTGTGCGAGGATGTGTATGAGAAGAGCTGTAGCCACCTTT 1557
Qy 861 TAAACCTCAAGTAATCTGTAGACAGATATAGATATATTTTGTATGAAGATTTACAGCTCA 920
Db 1558 CAAGCCCGAGGTCACTCTGTAGACTGTACACAGGTATTTTCATGAGGAGTTTACAGCTCA 1617
Qy 921 GACTATTACATAACACACCTGAAAAATATGA 953
Db 1618 GATGATCACCATCAAGCGCCTGTCAAGATGA 1650

RESULT 5
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RGS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1

Query Match 52.7%; Score 515.8; DB 3; Length 1599;
Best Local Similarity 72.0%; Pred. No. 2.5e-136;
Matches 673; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

Qy 19 AGAAGACAATGAATGATTTTGACTATTTGAACTACTAGTAAGGACCTTTTGGGAAA 78
Db 523 AAAGTGACCATGAATGATCTCGACTATCTCAAACTCTTGGCAAGGAAACCTTTGGCAAA 582
Qy 79 GTTATTTTGGTTCGAGAGGAGGCAAGTGAATAATACTATGCTATGAAGATTTCTGAAGAAA 138
Db 583 GTCATCTGTTGCGGGAGAGGCCACTGGCCGCTACTACGCCATGAAGATCTCTCGAAG 642
Qy 139 GAAGTCATATTGCAAGAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTATAAG 198
Db 643 GAAGTCATATTGCAAGAGATGAAGTGGCTCACACAGTCAAGAGAGCGGGTCTCCAG 702
Qy 199 AACACTAGACATCCCTTTTAAACATCTTGAATAATTCCTTCCAGACAAAGACCGTTTG 258
Db 703 AACACCAAGGACCGGTTCTCACTGCGCTGAAGTATGCTTTCCAGACCCACGACCGCTG 762
Qy 259 TGTTTTGTGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTGTTCGAGAGAGCGG 318
Db 763 TGTCTTGTGATGGAGTATGCCAAGGGGGTGAGCTGTCTTCCACCTGTCCGGGAGCGT 822
Qy 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATGTCTCTGCTTGGACTAT 378
Db 823 GTCTTTCAGAGAGGCGGGCCGGTTTATGTTGTCAGAGATTTGTCTCGGCTCTTGAGTAC 882
Qy 379 CTACATTCGGAAGATTTGTCTACGGTGATCTCAAGTTGGAGATCTAATGCTCGACAAA 438
Db 883 TTGCACTCGCGGGAGCGTGGTATACCGCGACATCAAGCTGGAACACCTCATGCTGGACAAA 942
Qy 439 GATGCCACATAAAAATTTACAGATTTTGGACTTTTGCAAAGAGGAGATCACAGATGCAGCC 498
Db 943 GATGCCACATCAAGATCACTGACTTTGGCCCTCTTGCAAGAGGGCATCAGTACGGGGCC 1002
Qy 499 ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTTGAAGATAAT 558
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Db 1003 ACCATGAAAACCTTCTGTGGGACCCCGGAGTACCTCTGGCGCTGAGGTGCTGGAGGACAA 1062
Qy 559 GACTATGGCGAGCAGTAGACTGTGTGGGGCTAGGGGTGTGTCATGTATGAAATGATGTGT 618
Db 1063 GACTATGGCGGGCGGTGGACTGTGTGGGGCTGGGTGTGGTTCATGTACGAGATGATGTGC 1122
Qy 619 GGGAGGTTACCTTTCTACAACCCAGGACCATGAGAAACTTTTGAATTAATTAATGAA 678
Db 1123 GGGCGCTGCTCTTCTACAACCCAGGACCATGAGGCGCTCTTCGAGCTCATCTCATGGAA 1182
Qy 679 GACATTAATTTCTCGAACACACTCTCTTCAGATGCAAAATCATTTCTCAGGCTCTTG 738
Db 1183 GAGATCCGCTTCCGCGCACGCTCAGCCCCGAGGCCAAGTCCCTGCTGTGGGTGCTT 1242
Qy 739 ATAAAGGATCCAAATAAACGCTTGTGGAGGACCATGATGATGCAAAAGAAATATATGAGA 798
Db 1243 AAGNAGGACCCCAAGCAGAGGCTTGTGGGGGCCAGCGATGCCAAGGAGTCAAGAG 1302
Qy 799 CACAGTTTCTTCTTGGAGTAAACTGCAAGATGTATATGATAAAAAGCTTTGTACCTCT 858
Db 1303 CACAGGTTCTTCTCAGCATCAACTGGCAGGACGTTGGTCCAGAGAAGAGCTCTGCCACCC 1362
Qy 859 TTTAAACCTCAAGTAACATCTGACAGACATCTAGATATTTTGAAGAAATTTACAGCT 918
Db 1363 TTTAAACCTCAGGTACGTCGAGGTCGACACCAAGGTACTTCGATGATGAATTTACCGCC 1422
Qy 919 CAGACTATTACAATAACACACCACTGAAAAATATGA 953
Db 1423 CAGTCCATCAATCACACCCCTGACCGCTATGA 1457

RESULT 6
US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

RESULT 7

Db 823 GTCATTACAGAGGACCGGCGCTTTTATGGTCAGAGATTGTCTGGCTCTTTGAGTAC 882
Qy 379 CTACATTCCGGAAGATTTGTACCGTGATCTCAAGTTGGAGATCTAAATCTCTGACAAA 438
Db 883 TTGCATCTCGGGACGTTGATATACCGGCACATCAAGCTGGAAACCTCATGCTGACAAA 942
Qy 439 GATGGCCACATAAAAATTTACAGATTTTGGACTTTTGGACTTTTGGCAAGAGGATCACAGATGACGCC 498
Db 943 GATGGCCACATCAAGATCACTGACTTTTGGCCCTCTGCAAGAGGACATCAGTGACGGGCC 1002
Qy 499 ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCAACAGAGGTGTTAGAGATAAT 558
Db 1003 ACCATGAAGACCTTTCTGTGGACCCCGAGTAGTCTGGCGCTCTGAGTGCTGGAGGACAA 1062
Qy 559 GACTATGGCCGACGAGTAGACTGTGTGGGCGCTTGGGCTGTGATGTATGAATGATGTGT 618
Db 1063 GACTATGGCCGCGGCTGGACTGTGTGGGCTGGGTGTGATGTATGATGATGATGTGC 1122
Qy 619 GGGAGGTTTACCTTTCTACAAACAGGACCATGAGAACTTTTGGAAATTAATTAATGAA 678
Db 1123 GGCGCGCTCCCTTCTACAAACAGGACCAACGAGCGCTCTTCGAGCTCATCTCATGAA 1182
Qy 679 GACATTAATTTCTCGAAGCTCTTCTCAGATGCAAAATCAITGCTTTTCAAGGCTCTTG 738
Db 1183 GAGATCCGCTTCCGCGCACGCTCAGCCCGAGCCAAAGTCCCTGCTGTGGGCTGCTT 1242
Qy 739 ATAAGGATCCAAATAAACGCTTGGTGAGGACCATGAGATGATGCAAAAGAAATTAATGAA 798
Db 1243 AAGAGGACCCCAAGCAGAGCTTGGTGGGGGCGCAGCATGCCAGGAGGTATGAG 1302
Qy 799 CACAGTTTCTTCTCGGAGTAACTGGCAAGATGTATATGATAAAAGCTTTGTACCTCCT 858
Db 1303 CACAGTTTCTTCTCAGCATCAACTGGCAGGACGTGGTCCAGAGAGCTCTCCACCC 1362
Qy 859 TTTAACTCTAAGTAACATCTGACAGATATCTAGATATTTTGTATGAAGAAATTTACAGCT 918
Db 1363 TTTAACTCTAAGTACGTCGAGGTGACACAAGGTACTTCGATGATGAATTTACCGCC 1422
Qy 919 CAGACTATTACAATAACACCACTTGAAATAATCA 953
Db 1423 CAGTCCATCAAAATACACACCCCTGACCGCTATGA 1457

RESULT 8
US-09-417-197-70
; Sequence 70, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; FILE OF INVENTION: On A Cellular Response
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2178)
US-09-417-197-70
Query Match 52.2%; Score 510.6; DB 3; Length 2181;
Best Local Similarity 72.5%; Pred. No. 8.5e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;
Qy 24 GACAATGAATGATTTTGACTATTGAAACTACTAGTAAAGGCACCTTTTGGGAAAGTTAT 83

Db 435 GACCATGAACGAGTTTGTAGTACCTTGAAGCTGCTGGGCAAGGGCACTTTTCGCAAGGTGAT 494
Qy 84 TTTGGTTTCGAGAGAGGCAAGTGGAAAATATCTATGCTATGAAGATTTCTGAAGAAAGAGT 143
Db 495 CTGGTGAAGAGAGAGGCCACAGGCCCTACTACGCCATGAAGATCTCAAGAAAGGAAGT 554
Qy 144 CATTATTGCAAAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTTTAAAGAACAC 203
Db 555 CATCGTGGCCAAAGGACGAGGTGGCCACACACTCACCGAGAACCGCGTCTCTGCAGAACTC 614
Qy 204 TAGACATCCCTTTTAAACATCCCTTGAATAATATTCCTTCCAGACAAAAGACCGTTTGTGTT 263
Db 615 CAGGACACCCCTTCTCTACAGCCCTTGAAGTACTCTTTCCAGACCCACGACCGCTCTGCT 674
Qy 264 TGTGATGGAATATGTTTAAATGGGGCGAGCTGTTTTTCCATTGTCGAGAGAGCGGGTGT 323
Db 675 TGTGATGGAATATGTTTAAATGGGGCGAGCTGTTTTTCCACTGTCGCGGAACTGTGTT 734
Qy 324 CTCTGAGGACCGCACACGTTTCTATGGTGAGAAATTTGCTCTGCTTGGACTATCTACA 383
Db 735 CTCGAGGACCGGCGCTTCTATGGCGCTGAGATTTGTCTAGCCCTGGACTACCTGCA 794
Qy 384 TTCGGAAAGA---TTGTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGACAAAGA 440
Db 795 CTCGGAAGAAACGTTGTTGACCGGGACCTCAAGCTGGAGAACCTCATGCTGGACAAGGA 854
Qy 441 TGGCCACATAAAAATTAACAGATTTTGACATTTTGCAAAAGAGGGATCACAGATGCAGCCAC 500
Db 855 CGGCGCATTAAGATACAGACTTCGGGCTGTGCAGAGGGGATCAAGACGTTGCCAC 914
Qy 501 CATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACACAGAGGTGTTAGAAGATAATGA 560
Db 915 CATGAAGACCTTTTGGGCGCACACTGAGTACCTGGCCCCCGAGGTGCTGGAGGACATGA 974
Qy 561 CTATGGCCGACGATAGACTGGTGGGCGCTAGGGGTTGTGATGTAATGAATGATGTGTTGG 620
Db 975 CTACGCGCTGACGTGACTGGTGGGCGCTGGGCGTGTGATGTAACGAGATGATGTGCGG 1034
Qy 621 GAGGTTACCTTTCTACACAGGACCATGAGAACTTTTGAATTAATATTAATGGAAGA 680
Db 1035 TCGCTGCCCTTTCTACAAACAGGACCATGAGAACTTTTGTGCTCATCTCTCATGGAGGA 1094
Qy 681 CATTAAATTTCTCGAACACTCTCTCAGATGCAAAATCATTTGCTTTCAGGGCTCTTGAT 740
Db 1095 GATCCGCTTCCGCGCACGCTTGGTCCGAGGCCAAGTCTCTGTTTTCAGGGCTGCTCAA 1154
Qy 741 AAAGGATCCAAATAAACGCTTGGTGAGGACCAAGATGATGCAAAAGAAATTTATGAGACA 800
Db 1155 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGAGCCCAAGGAGATCATGCAGCA 1214
Qy 801 CAGTTTCTTCTCTGGAGTAACTGGCAAGATGTATATGATAAAAGCTTGTACCTCCTTT 860
Db 1215 TCGCTTCTTTGGCGGTATCGTGTGGCAGCAGCTGTACGAGAAAGCTCAGCCCCACCTT 1274
Qy 861 TAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGTGAAAGAAATTTACAGCTCA 920
Db 1275 CAAGCCCCAGGTCACTGCGGAGACTGACAACAGGTATTTTGTGAGGAGTTTACGGGCCA 1334
Qy 921 GACTATTACAATAACACCACTGAAAAATATGA 953
Db 1335 GATGATCACCATCACACCACCTGACCAAGATGA 1367

RESULT 9
US-09-417-197-138
; Sequence 138, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0110P


```
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PKB fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138

Query Match      52.2%; Score 510.6; DB 3; Length 2184;
Best Local Similarity 72.5%; Pred. No. 8.5e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGATGATTTTGAATCTAGTAAAGCAGCTTTGGGAAAGTTAT 83
DB 1176 GACCATGACGAGTTTGAATCTAGTAAAGCAGCTTTGGGAAAGTTAT 1235
QY 84 TTTGGTTTCGAGAGAGGCAAGTGAATACTATCTGTAAGATCTGAAGAAAGT 143
DB 1236 CTTGGTGAAGGAGAGGCAAGTGAATACTATCTGTAAGATCTGAAGAAAGT 1295
QY 144 CATTTATGCAAAAGGATGAAGTGGCCACACACTTAAGTGAAGCAGAGTATTAAGAAACAC 203
DB 1296 CATCGTGGCCAGGAGTGGCCACACACTTAAGTGAAGCAGAGTATTAAGAAACAC 1355
QY 204 TAGACATCCCTTTTAAACATCTTGAATATCTTCCAGACAAAGACCGTTTGTGTTT 263
DB 1356 CAGGCACCCCTTCTCAGACCTGAAGTACTCTTCCAGACCCAGACCGCTCTGCTT 1415
QY 264 TGTGATGGAATATGTAAGTGGGGCGAGCTGTTTCCATTTGTCGAGAGCGGGTGT 323
DB 1416 TGTGATGGAATATGTAAGTGGGGCGAGCTGTTTCCATTTGTCGAGAGCGGGTGT 1475
QY 324 CTCTGAGGACCCGACACAGCTTTCTATGTCGAGAAATTTGTCTGCTTGGACTATCTACA 383
DB 1476 CTCTGAGGACCCGACACAGCTTTCTATGTCGAGAAATTTGTCTGCTTGGACTATCTACA 1535
QY 384 TTCCGGAAAGA--TTGTGTCACGTCATCTAAGTTGGAGAAATCTAATGCTGGACAAAGA 440
DB 1536 CTCCGAGAGAAAGCTGTTGTCACGAGCTCAAGCTGGAGAACTCTATCTGGACAAAGA 1595
QY 441 TGGCCACATAAATTAACAGATTTTGGACTTTTGAAGTGAAGGATCACAGATGCGCCAC 500
DB 1596 CCGGCACATTAAGATCACAGATTTTGGACTTTTGAAGTGAAGGATCACAGATGCGCCAC 1655
QY 501 CATGAAGACATTTCTGTCGACCTCCAGAAATCTGTCGACAGAGGTTTGAAGAAATGA 560
DB 1656 CATGAAGACATTTCTGTCGACCTCCAGAAATCTGTCGACAGAGGTTTGAAGAAATGA 1715
QY 561 CTATGCGCCGAGCAGTAGACTGTTGGGGCTTAGGGGTTGTCTATGTAATGATGTGG 620
DB 1716 CTATGCGCCGAGCAGTAGACTGTTGGGGCTTAGGGGTTGTCTATGTAATGATGTGG 1775
QY 621 GAGGTTACCTTTCTACAACACGAGCAATGAGAAATCTTTTGAATTAATTAATGAAGA 680
DB 1776 TCGCCTGCGCTTCTACAACACGAGCAATGAGAAATCTTTTGAATTAATTAATGAAGA 1835
QY 681 CATTAATTTCTCGAACAATCTCTTTCAGATGCAAAATCATTTGCTTACAGGCTCTTGAT 740
DB 1836 GATTCGCTTCCCGCGCAGCTTGGTCCGAGGCAAGTCTTCTGCTTTTACAGGCTCTGCTAA 1895
QY 741 AAAGGATCCAAATAAAGCGCTTGGTGGAGGACAGATGATGCAAAAGAAATATGAGACA 800
DB 1896 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCAAGGAGATCATGACGA 1955
QY 801 CAGTTTCTCTGAGAGTAACTGGCAAGATGATATGATTAAGAACTTGTACCTCTT 860
DB 860 CAGTTTCTCTGAGAGTAACTGGCAAGATGATATGATTAAGAACTTGTACCTCTT
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DB 1956 TCGCTTCTTTGGCGGTATCGTGTGCGACGACGTGTACGAGAAAGCTCAGCCACCCTT 2015
QY 861 TAAACCTCAAGTAAATCTGAGACAGATACCTAGATATTTTGTATGAAGAAATTTACAGCTCA 920
DB 2016 CAAGCCCGAGGTCAGCTCGGAGACTGACACACGAGTATTTTGTATGAGGAGTTTCAAGCCCA 2075
QY 921 GACTATTACAATAACACCACTGAAATAATGA 953
DB 2076 GATGATCACCATCACACCACTGACCAAGATGA 2108

RESULT 10
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Query Match      52.2%; Score 510.6; DB 2; Length 2610;
Best Local Similarity 72.5%; Pred. No. 9.2e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGATGATTTTGAATCTAGTAAAGCAGCTTTTGGGAAAGTTAT 83
DB 633 GACCATGACGAGTTTGAATCTAGTAAAGCAGCTTTTGGGAAAGTTAT 692
QY 84 TTTGGTTTCGAGAGAGGCAAGTGAATAATCTATCTATGAAGATTTCTGAAGAAAGAGT 143
DB 693 CTTGTTGAAGGAGAGGCAAGTGAATAATCTATCTATGAAGATTTCTGAAGAAAGAGT 752
QY 144 CATTTATGCAAAAGGATGAAGTGGCCACACACTTAAGTGAAGCAGAGTATTAAGAAACAC 203
DB 753 CATCTGCGCAAGGACGAGTGGCCACACACTTAAGTGAAGCAGAGTATTAAGAAACAC 812
QY 204 TAGACATCCCTTTTAAACATCTTGAATAATCTTCCAGACAAAGACCGTTTGTGTTT 263
DB 813 CAGGCACCCCTTCTCTACAGCCCTGAAAGTACTCTTTTCCAGACCCACGACCGCTCTGCTT 872
QY 264 TGTGATGGAATATGTTAATGSGGGGAGCTGTTTTCATTTGTCGAGAGAGCGGTGTT 323
DB 873 TGTGATGGAATATGTTAATGSGGGGAGCTGTTTTCATTTGTCGAGAGAGCGGTGTT 932
QY 324 CTCTGAGGACCCGACACAGCTTTCTATGTCGAGAAATTTGTCTGCTTGGACTATCTACA 383
DB 933 CTCCGAGGACCCGCGCCGCTTCTATGTCGAGTGTGTGTCAGCCCTGGACTACCTGCA 992
QY 384 TTCCGGAAAGA--TTGTGTACCGTGTATCTAAGTTGGAGAAATCTAATGCTGGACAAAGA 440
DB 993 CTCCGAGAGAAAGCTGTGTGTACCGGACCTCAAGCTGGAGAACTCTATCTGGACAAAGA 1052
QY 441 TGGCCACATAAATTAACAGATTTTGGACTTTTGAAGTGAAGGAGGATCACAGATGCGCCAC 500
DB 1053 CCGGCACATTAAGATCACAGACTTCCGAGTGTGCAAGGAGGGGATCAAGACGCTGCCAC 1112
QY 501 CATGAAGACATTTCTGTCGACCTCCAGAAATCTTGGCACCAGAGGTTTGAAGAAATGA 560
DB 1113 CATGAAGACATTTCTGTCGACCTCCAGAAATCTTGGCACCAGAGGTTTGAAGAAATGA 1172
QY 561 CTATGCGCGAGCAGTAGACTGTTGGGGCTTAGGGGTTGTCTATGTAAGAAATGATGTGG 620
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Db 1173 CTACGGCGGTGACGTGGACTGGTGGGGCTGGGGCTGGTCTATGTACGAGATGATGTGGG 1232
Qy 621 GAGGTATCTTCTACACACAGGACCATGAGAACTTTTGAATTAATTAATTAATGAAGA 680
Db 1233 TCGCTGCGCTTCTACACACAGGACCATGAGAACTTTTGAAGCTTATCTCTCATGGAGGA 1292
Qy 681 CATTAATAATTTCTCGAACACATCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCTTGAT 740
Db 1293 GATCGCTTCCCGCGCAGCTTGGTCCGAGGCCAAGTCCTTCTTTCAGGGCTGCTCAA 1352
Qy 741 AAAGATCCAAATAAAGCCCTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGACA 800
Db 1353 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGGAGATCATGCAGCA 1412
Qy 801 CAGTTTCTTCTCGAGTAAACTGCGAAGATGTATATGATAAAAGCTTGTACCTCTCTT 860
Db 1413 TCGCTTCTTCCCGGTATCGTGTGGCAGCAGTGTACGAGGAAGCTTCAGCCCAACCTT 1472
Qy 861 TAAACCTCAAGTAACATCTGAGACAGATACATAGATATTTTGAAGAATAATTAACAGCTCA 920
Db 1473 CAAGCCCGAGTCAAGTCGGAGACTGACACAGGTATTTTATGAGGAGTTTCACGGCCA 1532
Qy 921 GACTATTACATAACACACCTGAAATAATGA 953
Db 1533 GATGATCACCATCACACCCTGACCAAGATGA 1565

RESULT 11

US-09-081-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemming, Brian A.
; APPLICANT: Frech, Matthias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091,058
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1

Query Match 52.2%; Score 510.6; DB 3; Length 2610;
Best Local Similarity 72.5%; Pred. No. 9.2e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;
Qy 24 GACAAATGATGATTTGACTATTTGAAACTACTAGTTAAAGGCACTTTTGGGAAAGTTAT 83
Db 633 GACCATGAACGAGTTGAGTACCTGAAAGCTGCTGGCAAGGGCACTTTTCGGCAAGGTGAT 692
Qy 84 TTTGGTTCGAGAGAGGCAAGTGAATAATCTATGCTATGAAGATCTGGAAGAAAGAT 143
Db 693 CTGCTGAGAGAGAGGCAAGGCGGCTACTAGCCATGAGATCTCAGAGAGGAGT 752
Qy 144 CATTTATGCAAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTTAAAGAACAC 203
Db 753 CATCGTGGCCAAAGCAGAGTGGGCCACACACTCACGAGAACCGCTCTCGCAGAACTC 812
Qy 204 TAGACATCCCTTTTAACTATCTTGAATAATCTTCCAGCAAAAGACCGTTGTGTTT 263
Db 813 CAGGACCCCTTCTCAAGCCCTGAAAGTACTCTTTCCAGACCACGACCGCCTCTGCTT 872

Qy 264 TGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTTGTGAGAGAGCGGGTGT 323
Db 873 TGTGATGAGTACGCCAAACGGGGCGAGCTGTTCTTCCACTGTCCCGGGAACGCTGTGT 932
Qy 324 CTCTGAGGACCGCACAGCTTTCTATGTGAGAAATTTGTCTCTGCCCTTGGACTATCTACA 383
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Qy 384 TTCGGGAAAGA---TTGTGTACCGTGTATCTCAAGTTGGAGAACTAATCTGCTGGCAAGA 440
Db 993 CTCGGAAGAAACGTTGTGTACCGGGACCTCAAGCTGGAGAACCTCATGCTGGACAAGGA 1052
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Db 1113 CATGAAGACCTTTTGGCGCACACCTGAGTACCTGGCCCGGAGGTGCTGGAGGACAATGA 1172
Qy 561 CTATGGCCGAGCAGTACAGCTGGTGGGCTAGGGCTTGTGATGATGAAATGATGTGG 620
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Qy 681 CATTAATAATTTCTCGAAACATCTCTTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCTTGAT 740
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Qy 741 AAAGGATCCAAATAAAGCCCTTGGTGGAGGACAGATGATGCAAAAGAAATTAAGAGACA 800
Db 1353 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGGAGATCATGCAGCA 1412
Qy 801 CAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTTGTACCTCTCTT 860
Db 1413 TCGCTTCTTTCGGGTATCGTGTGGCAGCAGCTGTACGAGAGAAAGCTCAGCCCACTT 1472
Qy 861 TAAACCTCAAGTAACTCTGAGACAGATACATAGATATTTTGAAGAATAATTAAGCTCA 920
Db 1473 CAAGCCCGAGTCAAGTGGAGACTGACACAGGTATTTTATGAGGAGTTTCAGGGCCA 1532
Qy 921 GACTATTACATAACACACCTGAAATAATGA 953
Db 1533 GATGATCACCATCACACCCTGACCAAGATGA 1565

RESULT 12

US-09-023-655-1206
; Sequence 1206, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g190827
; US-09-023-655-1206

Query Match 52.2%; Score 510.6; DB 3; Length 2610;
Best Local Similarity 72.5%; Pred. No. 9.2e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGAATGATTTGACTATTGAACTACTAGTAAAGCACATTTTGGGAAAGTTAT 83
DB 633 GACCATGACGAGTTTGAGTACCTGAAGCTGTGGGCAAGGCACATTTGGGCAAGGTGAT 692
QY 84 TTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTTCTGAAAGAAAGT 143
DB 693 CCTGGTGAAGGAGAGGCAAGGCACAGGCGGCTACTACGCCATGAAGATCCTCAAGAGGAAGT 752
QY 144 CATATTGCAAAAGGATGAAGTGGGCAACACTTAAGTAAAGGCACTTTTGGGAAAGTTAT 263
DB 753 CATCGTGGCAAGGACGAGGTGGCCCAACACTACCGGAAACCGCGCTCTCGAAGACTC 812
QY 204 TAGACATCCCTTTTAAACATCTTGAATATATCTTCCAGACAAAGACCGTTTGTGTT 263
DB 813 CAGGACCCCTTCTTCACAGCCCTGAAGTATCTTTTCAGACCCACGACCGGCTCTGCTT 872
QY 264 TGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTTGTGCGAGAGAGCGGTGTT 323
DB 873 TGTGATGAGTACGCCAACCGGGGCGAGCTGTTCTTCCACCTGTCCCGGAAAGCTGTGTT 932
QY 324 CTCTGAGGACCGCACACGTTTCTATGTTGCGAAGAAATTTGTCTCTGCGCTTGGACTATCTACA 383
DB 933 CTCCGAGGACCGGGCCCGCTTCTATGGGCGTGAAGTGTGTGTCAGGCTTGGACTACCTGCA 992
QY 384 TTCCGGGAAGA---TTGTTGTAACCGGTGATCTCAAGTTGGAGATCTAACTCTGACAAAGA 440
DB 993 CTCGGAGAGAAACGTTGTTACCGGACCTCAAGCTGGGAAACCTCATCTCGAAGGA 1052
QY 441 TGGCCACATAAAATTAACAGATTTTGGACTTTGCAAGAGGGAACACAGATGCGAGCCAC 500
DB 1053 CCGGCACATTAAGATCAGAGATCTGGGCTGTGCAAGGAGGGGATCAAGGACGGTGCCAC 1112
QY 501 CATGAAGACATTTCTGGGCACTCCAGAAATATCTGGCACAGAGGTTGTTAGAAGATAATGA 560
DB 1113 CATGAGACATTTTGGGCAACACTGAGTACTGGCCCCGAGGTGCTGGAGGACATGA 1172
QY 561 CTATGCCCCGAGTAGATCTGTGGGCGCTAGGGGTTGTATGATGAAATGATGTGTGG 620
DB 1173 CTACGGCCGTGAGTGAATGAGTGGGGCTGGGCGTGGTCAATGACAGATGATGTGGC 1232
QY 621 GAGGTACTCTTTACAAACAGGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
DB 1233 TCGCCTGGCCCTTCTACAAACAGGACCATGAGAACTTTTGGAGCTCATCTCATGGAGGA 1292

RESULT 13
US-09-590-740-1
; Sequence 1, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; TITLE OF INVENTION: HMV CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-590-740-1

Query Match 52.2%; Score 510.6; DB 3; Length 2610;
Best Local Similarity 72.5%; Pred. No. 9.2e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGAATGATTTGACTATTGAACTACTAGTAAAGCACATTTTGGGAAAGTTAT 83
DB 633 GACCATGACGAGTTTGAGTACCTGAAGCTGTGGGCAAGGCACATTTGGGCAAGGTGAT 692
QY 84 TTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTTCTGAAAGAAAGT 143
DB 693 CCTGGTGAAGGAGAGGCAAGGCACAGGCGGCTACTACGCCATGAAGATCCTCAAGAGGAAGT 752
QY 144 CATATTGCAAAAGGATGAAGTGGGCAACACTTAAGTAAAGGCACTTTTGGGAAAGTTAT 263
DB 753 CATCGTGGCAAGGACGAGGTGGCCCAACACTACCGGAAACCGCGCTCTCGAAGACTC 812
QY 204 TAGACATCCCTTTTAAACATCTTGAATATATCTTCCAGACAAAGACCGTTTGTGTT 263
DB 813 CAGGACCCCTTCTTCACAGCCCTGAAGTATCTTTTCAGACCCACGACCGGCTCTGCTT 872
QY 264 TGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTTGTGCGAGAGAGCGGTGTT 323
DB 873 TGTGATGAGTACGCCAACCGGGGCGAGCTGTTCTTCCACCTGTCCCGGAAAGCTGTGTT 932
QY 324 CTCTGAGGACCGCACACGTTTCTATGTTGCGAAGAAATTTGTCTCTGCGCTTGGACTATCTACA 383
DB 933 CTCCGAGGACCGGGCCCGCTTCTATGGGCGTGAAGTGTGTGTCAGGCTTGGACTACCTGCA 992
QY 384 TTCCGGGAAGA---TTGTTGTAACCGGTGATCTCAAGTTGGAGATCTAACTCTGACAAAGA 440
DB 993 CTCGGAGAGAAACGTTGTTACCGGACCTCAAGCTGGGAAACCTCATCTCGAAGGA 1052
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Qy 441 TGGCCACATAAAATTACAGATTTTGGACTTTTGAACATTTGCAAGAGAGGATCACAGATGAGCCAC 500
Db 1053 CGGACACATTAAAGATTCAGACTTCGGGCTGCAAGAGAGGGATCAAGAGCGGTGCCAC 1112
Qy 501 CATGAAGACATTCGTGGCACTCAGAAATATCTGGCACAGAGGTGTTAGAAGATATGA 560
Db 1113 CATGAAGACCTTTTTCGGGCACACCTGAGTACTTGGCCCCCGAGGTGCTGGAGGACAATGA 1172
Qy 561 CTATGGCGGAGCAGTAGACTGCTGGGGCTAGGGGTTGTCAATGTAATGAATGATGCTGG 620
Db 1173 CTACGGCGCTGAGTGGTGGGGCTGGGGCTGGGGCTGATGACGAGATGATGTCGG 1232
Qy 621 GAGGTTACCTTTCTACACAGGACCATGAGAACTTTTGAATTAATTAATTAATGAAGA 680
Db 1233 TCGGCTGCCCTTCTACACAGGACCATGAGAACTTTTGGAGCTCATCTCATGGAGGA 1292
Qy 681 CATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTCAGGGCTCTTGAT 740
Db 1293 GATCCGCTTCCCGGCGACGCTTGGTCCGAGGCCAAGTCTTGTCTTTCAGGGCTGCTCAA 1352
Qy 741 AAAGGATCCAAATAAAGCCCTTGGTGGAGGACCATGATGCAAAAGAAATTAAGACA 800
Db 1353 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGAGCCCAAGGAGATCATGCGACA 1412
Qy 801 CAGTTTCTTCTCGGAGTAAACTGGCAAGATGATATGATAAAAGCTTGTACCTCCTTT 860
Db 1413 TCGCTTCTTTCGGGTATCGTGTGCGACAGCTGTACGAGNAGAGCTCAGGCCACCTTT 1472
Qy 861 TAAACCTCAAGTAACATCTGAGACAGATACATAGATATTTTATGAAGAAATTAACAGTCA 920
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Qy 921 GACTATTACATACACACCTGAAATATGA 953
Db 1533 GATGATCACCATCACACCCTGACCAAGATGA 1565
RESULT 14
US-09-590-740-3
; Sequence 3, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-3
Query Match 50.4%; Score 493; DB 3; Length 1254;
Best Local Similarity 72.0%; Pred. No. 6.7e-130;
Matches 672; Conservative 0; Mismatches 255; Indels 6; Gaps 2;
Qy 24 GACAAATGAATGATTTGACTATTTGAACTACTAGGTAAGGCACTTTTGGAAAGTTAT 83
Db 249 GACCATGAACGAGTTGAGTACCTGAGCTCTGGGCAAGGCACTTTCGCAAGGTGAT 308
Qy 84 TTTGGTTCCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTTCTGAAGAAAGAGT 143
Db 309 CCTGGTGAAGGAGAGGCAAGCG---TACTAGCCATGAAGATCCTCAAGAGGAAGT 365
Qy 144 CATTTATGCAAGGATGAGTGGGACACACTCTAATCTGAAAGCAGAGATTAAGAACAC 203
Db 366 CATCGTGGCCCAAGGACGAGGTGGGCCACACACTCACCGAGAACCGCGTCCAGCAGAACTC 425

Qy 204 TAGACATCCCTTTTAAACATCCTTGAATATTCCTTCCAGACAAAGACCGCTTGTGTTT 263
Db 426 CAGGACCCCTTCTCTCACTCGCTGAACTACTCTTTCCAGACCCACCGCTCTGCTT 485
Qy 264 TGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTGTCGAGAGAGCGGGTGT 323
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Db 726 CATGAAGACCTTTTGGCGCACACCTGAGTACCTTGGCCCCCGAGGTGCTGGAGGACAAATGA 785
Qy 561 CTATGGCGGAGCAGTAGACTTGGTGGGCTTAGGGTTGTCTATGTATGAAATGATGTGTGG 620
Db 786 CTACGGCGGTGAGTGGACTTGGTGGGGCTTGGGGCTGCTGATGAGATGATGTGCGG 845
Qy 621 GAGGTTACCTTTCTACAAACAGGACCATGAGAACTTTTGAATTAATTAATGAAGA 680
Db 846 TCGCTGCCCTTCTACAAACAGGACCATGAGAACTTTTGAATTAATTAATGAAGA 905
Qy 681 CATTAATTTCTCGAACACTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTTGTAT 740
Db 906 GATCCGCTTCCCGCGCACGCTTGGTCCGAGGCCAAGTCTTGTCTTTCAGGGCTGCTCAA 965
Qy 741 AAAGGATCCAAATAAAGCCCTTGGTGGAGGACCATGATGCAAAAGAAATTAAGACA 800
Db 966 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGGAGATCATGCGACA 1025
Qy 801 CAGTTTCTTCTGAGGATAAACTGGCAAGATGATATGATGATAAAAGCTTGTACCTCTTT 860
Db 1026 TCGCTTCTTTCAGCGGTATCGTGTGGCAGCAGTGTACGAGAAAGCTCAGCCACCTT 1085
Qy 861 TAAACCTCAAGTAACTCTGAGACAGATACATAGATATTTTGAATGAAGAAATTAAGACTCA 920
Db 1086 CAAGCCCGGCTCAGCTCGGAGACTGACACAGGTATTTTATGAGGAGTTTACGGCCCA 1145
Qy 921 GACTATTACAAATAACACCACTCGAAAAATATGA 953
Db 1146 GATGATCACCATCACACCACCTGACCAAGATGA 1178

RESULT 15
US-09-474-922A-2
; Sequence 2, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowbert
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2

Query Match 39.2%; Score 383.8; DB 3; Length 387;
Best Local Similarity 99.5%; Pred. No. 4.3e-99;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 617 GTGGGAGGTTACCTTTCTACAAACAGGACCATGAGAACTTTTGAATTAATTAATGG 676
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Db 61 GTGGGAGGTTACCTTTCTACAAACAGGACCATGAGAACTTTTGAATTAATTAATGG 120
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QY 677 AAGACATTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTGCTTCAGGGCTCT 736
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Db 121 AAGACATTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTGCTTCAGGGCTCT 180
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QY 737 TGATAAAGGATCCAAATAAAACGCTTTGGTGGAGGACCCAGATGATCAAAAAGAAATTATGA 796
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Db 181 TGATAAAGGATCCAAATAAAACGCTTTGGTGGAGGACCCAGATGATCAAAAAGAAATTATGA 240
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QY 797 GACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAAGCTTGTACCTC 856
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Db 241 GACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAAGCTTGTACCTC 300
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QY 857 CTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTTTCATGAAGAAATTACAG 916
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Db 301 CTCCTAAACCTCAAGTAACTCTGAGACAGATAGATATTTTTCATGAAGAAATTACAG 360
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QY 917 CTCAGACTATTACAATAACACCACCTG 943
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Db 361 CTCAGACTATTACAATAACACCACCTG 387
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Perfect score: 978

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 12494176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	861.4	88.1	1548	11	US-11-136-527-2356
3	525	53.7	1443	11	US-11-170-693-66
4	517	52.9	2349	11	US-11-136-527-2338
5	516.2	52.8	1617	11	US-11-136-527-1823
6	515.8	52.7	1715	7	US-10-947-249-56
7	401.8	41.1	600	11	US-11-136-527-7052
8	269.6	27.6	3201	11	US-11-136-527-4033
9	258.8	26.5	3206	7	US-10-821-234-306
10	253.6	25.9	2453	11	US-11-136-527-2486
11	246.4	25.2	3017	11	US-11-000-688-1184
12	236.4	24.2	2615	11	US-11-136-527-2878
13	229.8	23.5	5537	11	US-11-152-366-2
14	229.4	23.5	3075	11	US-11-136-527-1950
15	226.4	23.1	2146	7	US-10-955-054-34
16	223	22.8	3524	11	US-11-136-527-3329
17	222.4	22.7	2346	11	US-11-117-013-3
18	222.4	22.7	2346	11	US-11-000-688-1538
19	219	22.4	1800	11	US-11-136-527-3715
20	216.8	22.2	3186	7	US-10-995-561-339
21	216.8	22.2	3242	7	US-10-995-561-338

ALIGNMENTS

RESULT 1

US-10-826-585-45
; Sequence 45, Application US/10826585
; Publication No. US20060008807A1
; GENERAL INFORMATION:
; APPLICANT: Immunivest Corporation
; APPLICANT: O'Hara, Shawn Mark
; APPLICANT: Foulk, Brad
; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and
; TITLE OF INVENTION: morphological features on the same sample
; FILE REFERENCE: IMC 143 PCT/US
; CURRENT APPLICATION NUMBER: US/10/826,585
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 60/369945
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/330669
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/26867
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Human
US-10-826-585-45

Query Match 100.0%; Score 978; DB 6; Length 1547;

Best Local Similarity 100.0%; Pred. No. 2.8e-260; Mismatches 0; Indels 0; Gaps 0;

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QY	61	AAAGGACATTTGGGAAAGTTATTTTGGTTGAGAGAGGCAAGTGGAAAACTACTAGGT	120
DB	476	AAAGGACATTTGGGAAAGTTATTTTGGTTGAGAGAGGCAAGTGGAAAACTACTAGGT	535
QY	121	ATGAAGATTCTGAAGAAAGAGTCAATTTGCAAAAGGATGAAGTGGCACACACTCTAACT	180
DB	536	ATGAAGATTCTGAAGAAAGAGTCAATTTGCAAAAGGATGAAGTGGCACACACTCTAACT	595

Sequence 2369, Ap
Sequence 3070, Ap
Sequence 4035, Ap
Sequence 5919, Ap
Sequence 1949, Ap
Sequence 344, App
Sequence 37, Appl
Sequence 15, Appl
Sequence 32, Appl
Sequence 3389, Ap
Sequence 491, App
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Sequence 533, App
Sequence 1805, Ap
Sequence 270, App
Sequence 2671, Ap
Sequence 2887, Ap
Sequence 1709, Ap
Sequence 5351, Ap
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Sequence 6045, Ap
Sequence 1021, Ap
Sequence 1021, Ap

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Qy 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAATCCTTTGAAATATTCCTTC 240
Db 596 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAATCCTTTGAAATATTCCTTC 655
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTC 300
Db 656 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTC 715
Qy 301 CATTTGTGCGAGAGCGGGTCTCTCTGAGACCGCACACGTTTCTATGGTCGAGAAATT 360
Db 716 CATTTGTGCGAGAGCGGGTCTCTCTGAGACCGCACACGTTTCTATGGTCGAGAAATT 775
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db 776 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 835
Qy 421 AATCTAATGCTGGCAAGATGGCCACATAAABATTACAGATTTTGGACTTTGCAAGAA 480
Db 836 AATCTAATGCTGGCAAGATGGCCACATAAABATTACAGATTTTGGACTTTGCAAGAA 895
Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 896 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 955
Qy 541 GAGGTGTTAGAAATATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db 956 GAGGTGTTAGAAATATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015
Qy 601 ATGTATGAATGATGTGGGAGGTACCTTTCTACACCGAGGACCATGAGAACTTTTT 660
Db 1016 ATGTATGAATGATGTGGGAGGTACCTTTCTACACCGAGGACCATGAGAACTTTTT 1075
Qy 661 GAAATTAATTAATGAAGACATTAATTTCTCGAACACTCTCTCAGATGCAAAATCA 720
Db 1076 GAAATTAATTAATGAAGACATTAATTTCTCGAACACTCTCTCAGATGCAAAATCA 1135
Qy 721 TTGCTTTTCAGGCTCTTTGATAAAGATCCAAATAAACGCCCTTGTGGAGGACCAAGATGAT 780
Db 1136 TTGCTTTTCAGGCTCTTTGATAAAGATCCAAATAAACGCCCTTGTGGAGGACCAAGATGAT 1195
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 840
Db 1196 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 1255
Qy 841 AAAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTT 900
Db 1256 AAAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTT 1315
Qy 901 GATGAAGAAATTCAGCTCAGACTATTACAAATAACACCCTGAAATAATGATGAGGAT 960
Db 1316 GATGAAGAAATTCAGCTCAGACTATTACAAATAACACCCTGAAATAATGATGAGGAT 1375
Qy 961 GGTATGACTCGATGGAC 978
Db 1376 GGTATGACTCGATGGAC 1393
```

RESULT 2

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US-11-136-527-2956
; Sequence 2956, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136.527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2956
```

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; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2956
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Query Match 88.1%; Score 861.4; DB 11; Length 1548;
Best Local Similarity 94.1%; Pred. No. 4.5e-228;
Matches 895; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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Qy 1 TCTACACCCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT 60
Db 452 TCTACACCCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT 511
Qy 61 AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120
Db 512 AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 571
Qy 121 ATGAAGATTTCTGAAGAAAGAGTCATTTTGCAAAGGATGAAGTGGCACACACTCTAACT 180
Db 572 ATGAAGATTTCTGAAGAAAGAGTCATTTTGCAAAGGATGAAGTGGCACACACTCTAACT 631
Qy 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240
Db 632 GAGACAGAGTCTTAAAGAAACACACAGACATCCATTTCTAAACATCCTTTGAAATATTCCTTC 691
Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 300
Db 692 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 751
Qy 301 CATTTGTGCGAGAGCGGGTCTCTGAGGACCGCACACGTTTCTATGGTCGAGAAATT 360
Db 752 CATTTGTGCGAGAGCGGGTCTCTGAGGACCGCACACGTTTCTATGGTCGAGAAATT 811
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db 812 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 871
Qy 421 AATCTAATGCTGGCAAAAGATGGCCACATATAAATAATACGATTTTGGACTTTTGCAGAA 480
Db 872 AATCTAATGCTAGTAAGGATGGCCATATAAATAATACGATTTTGGACTTTTGCAGAA 931
Qy 481 GGGATCACAGATGCAGCCACCATGAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 932 GGGATCACAGATGCAGCTACCATGAAGACATTTCTGTGTTACACAGAGTATCTGGCACCA 991
Qy 541 GAGGTGTTAGAAATATGACTATGGCCGAGCTGTGGACTGGTGGGCGCTAGGGTGTGC 600
Db 992 GAGGTATTAAGAAATATGACTATGGCCGAGCTGTGGACTGGTGGGCGCTAGGGTGTGC 1051
Qy 601 ATGTATGAATGATGTGTGGAGGTTACCTTTCTACAAACGAGGACCAATGAGAACTTTTT 660
Db 1052 ATGTATGAATGATGTGTGGAGGTTGCTTTCTACAAACGAGGATCATGAGAACTCTTT 1111
Qy 661 GAATTAATATTAATGGAAGACATTAATTTCTCGAAACATCTCTTCAGATGCAAAATCA 720
Db 1112 GAACTAATACTCATGGAAGACATCAAAATTTCCCGCAACACTCTCTTCAGATGCAAAATCA 1171
Qy 721 TTGCTTTTCAGGCTCTTTGATAAAGGATCCAAATAAACGCCCTTGTGGAGGACCAAGATGAT 780
Db 1172 TTGCTTTTCAGGCTCTTTGATAAAGGATCCAAATAAACGCCCTTGTGGAGGCGGAGATGAT 1231
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840
Db 1232 CCAAGAGATATATGAGGACACAGTTTCTTTCTGGAGTAACTGGCAGGACGATATATGAC 1291
Qy 841 AAAAAGCTTGTACTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 900
Db 1292 AAAAAGCTTGTACTCTCTTTTAAAGCTCAAGTAACTCTGAGACAGACACAGATATTTT 1351
Qy 901 GATGAAGAAATTTACAGCTCAGACTTTTACAAATACACCACTGAAATAT 951
Db 1352 GATGAAGAAATTTACAGCTCAGACTTTTACAAATACACCACTGAAAGTGT 1402
```



```
RESULT 3
US-11-170-693-66
; Sequence 66, Application US/111170693
; Publication No. US20060014186A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Timothy A.
; TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING OF A STRAIN DISPOSED ON AN
; TITLE OF INVENTION: ABSORBENT CARRIER
; FILE REFERENCE: 023131.41500
; CURRENT APPLICATION NUMBER: US/11/170,693
; CURRENT FILING DATE: 2005-06-29
; PRIOR APPLICATION NUMBER: 60/230,371
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 09/945,952
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 11/074,995
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 11/
; PRIOR FILING DATE: 2005-06-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Mus sp.
US-11-170-693-66

Query Match      53.7%; Score 525; DB 11; Length 1443;
Best Local Similarity 73.4%; Pred. No. 3.5e-135;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

QY 24 GCAATGAATGATTTTGAATTTGAACTACTAGTAAAGGCACCTTTTGGGAAAGTTAT 83
DB 435 GACCATGAACGATTTGAGTACTGAACTACTGGCAAGGCACCTTTGGGAAAGTTAT 494
QY 84 TTTGGTTCAGAGAGAGGCAAGTGGAAAACTATGCTATGAAGATCTCGAAAGAAAGT 143
DB 495 TCTGGTGAAGAGAGAGCCACAGCCGCTACTATGCCATGAAGATCTCAAGAAAGGAGT 554
QY 144 CATTATTGCAAGGATGAAGTGCACACACTCTAACTGAAGCAGAGTATTAAAGAACAC 203
DB 555 CATCTGCGCAAGGATGAGTTGCCACACAGCTTACTGAGAACCGTGCTCGAGAACCTC 614
QY 204 TAGACATCCCTTTTAACTATCTTGAATATCTCTTCCAGACAAAAGACCGTTTGTGTTT 263
DB 615 TAGGCATCCCTTCTTACGCGCTCAAGTACTCATCTCCAGACCCACGCGCTCTGCTTT 674
QY 264 TGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCATTTGTCAGAGAGCGGGTGT 323
DB 675 TGTCTAGGAGTATGCCAACCGGGGCGAGCTCTTTTCCACCTGTCTCGAGAGCGCGTGT 734
QY 324 CTCTGAGGACCGCACACGTTCTATGGTCAGAAATTTGCTGCTGCTTGGACTATCTACA 383
DB 735 CTCGAGGACCGGGCGCGCTTCTATGGTCGAGATTTGTCTGCTTGGACTATCTGCA 794
QY 384 TTCCGGAAGA---TTGTGTACCGTGATCTCAAGTTGGGAATCTAATGCTCGACAAAGA 440
DB 795 CTCGAGAGAGACGTGTGTGTCGCGGACCTGAAGCTGGAGACCTCATCTCGACAAAGA 854
QY 441 TGCCACATAAAATTTACAGATTTTGGACTTTTGCAGAAAGAGGATCACAGATGCGAGCCAC 500
DB 855 CGGGCACATCAGATTAACGACTTCGGGCTGCAAGAGGGGATCAAGGATGGTCCAC 914
QY 501 CATGAGACATTTCTGGGCACTCCAGAAATCTGGCACCGAGGTTTGAAGATATGA 560
DB 915 TATGAAGACATCTCGGGAACCGCGAGTACCTGGCCCTTGAGGTGCTGGAGAACCA 974
QY 561 CTATGCCCGAGCAGTAGCTGTTGGGCGCTTAGGGGTTGTGATGTAATGATGTGG 620
DB 975 CTACGGCCGTCAGTGCAGTGTGTGGGGGCTGGGCGTGTGTCATGATGATGATGTGG 1034
QY 621 GAGGTTACCTTTCTACAAACAGGACCATGAGAAACCTTTTGAATTAATTAATGAAGA 680

RESULT 4
US-11-136-527-2338
; Sequence 2338, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2338
; LENGTH: 2349
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2338

Query Match      52.9%; Score 517; DB 11; Length 2349;
Best Local Similarity 71.3%; Pred. No. 6.8e-133;
Matches 667; Conservative 9; Mismatches 259; Indels 0; Gaps 0;

QY 19 AGAAAGACAATGAATGATTTTGACTATTTTGAACCTACTAGGTAAAGGCACCTTTTGGGAAA 78
DB 717 AAAGTGACCATGAACGACTTCGATTATCTCAAACTCTCGCAAGGGCACCTTCGGCAAA 776
QY 79 GTTATTTTGGTCGAGAGAGGCAAGTGGAAATACTATGCTATGAGATTTCTGAGAAA 138
DB 777 GTCATTTCTAGTTTCGAGAGAGAGGCCACTGGCCGCTATTATGCCATGAAGATCTGTGGAAG 836
QY 139 GAAGTCATTATTGCAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTATAAG 198
DB 837 GAGGTATCATTTGCAAGGATGAAGTGGCCCAACAGTCACAGAGAGCGAGTCTCTACAG 896
QY 199 AACACTAGACATCCCTTTTAAATCATCTTTTGAATAATTCCTTCCAGACAAAGACCGTTTG 258
DB 897 AATACAGGACCCCTTTCCTTACAGCCCTGAAGTATGCCCTTCAGACCCATGACCCCTG 956
QY 259 TGTTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTCCATTTGTGAGAGAGCGG 318
DB 957 TGTCTTGTGATGGAGTATGCCAACGGGGCGGAGCTGTTTTTCCACCTCTCTCGGAGCGA 1016
QY 319 GTGTTCTCTGAGGACCGCACAGCTTCTATGTCGAGAAATTTGTCTGCTTGGACTAT 378
DB 1017 GTCTTACGAGGAGTGGGACGCTTTATGAGGAGAGATTGTGTGAGGTAC 1076
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Qy	379	CTA	CATTCCGGAAAGA	TTGTGTA	CCGTGAT	CTCAAGTTGGAGAA	TCTAA	TGCTGGACAA	438
Db	1077	TTG	CAC	TGCGASGGAT	TGTGGT	GTACCGCGACAT	CAAGCTGGAAAA	ACCTTATGCTGGACAA	1136
Qy	439	GAT	GGCCACATAAAA	TTTACAGAT	TTTGGAC	TTTTCGAAA	GAAGGATC	CACAGATCGACCC	498
Db	1137	GAT	GGCCACATCA	AGATC	ACTTGACT	TTTGGCTTT	TGSCAAGAGGCGAT	CAGTGATGGGGCC	1196
Qy	499	ACC	ATGAAGACAT	TTCTGTGG	CAC	TCCAGAAT	TATCTGG	CACACAGAGGTGTTAGAA	558
Db	1197	ACC	ATGAACCTT	STGTGTG	ATCCCGG	AGTACTTGG	CGCCTGAGG	TGCTAGAGGACAT	1256
Qy	559	GAC	TATGGCCGAC	GACGAT	PAGACTGGT	GGGGCC	TAGGGTGTG	TATGTAAGAA	618
Db	1257	GAM	TACGGCGCTG	CAGTGG	ACTGGG	CGTGGT	CATGTAC	GATCATGTGC	1316
Qy	619	GGG	AGGTTACCTTT	CTACAAC	CCAGGAC	CATGAGAA	CTTTTGGAA	TTTAATTAATCGAA	678
Db	1317	GGC	CGCTGCCCTT	CTACAAC	CCAGGAC	CCAGGCGCTT	TCGAGCTCAT	CCTCATGGAG	1376
Qy	679	GAC	ATTAATTTCT	CTCGAA	CACTCTT	TCAGATG	CAAAATCAT	TTCCTTTCAGGGCTCTTG	738
Db	1377	GAG	ATCCGGTTC	CCACGAC	CGCTTGG	CCGACAGG	CCGACAGTCCCT	TGCTGGCTGGACTGCTC	1436
Qy	739	ATA	AGGATCCAA	TAAAC	CGCTTGGT	GGAGGA	CCAGATGAT	CAAAAGAAATPATGAGA	798
Db	1437	AAG	AGGACCCYAA	GACAGAG	CTCGTGG	GGGTCC	CAGTGATG	TCMAAGGAGGT	1496
Qy	799	CAC	AGTTTCTTCT	CTCGNGT	TAACTGGC	AGATGTATATG	TATATAAA	AGCTTGATACCTTCT	858
Db	1497	CAT	CGGTTCTTCT	CTCAGCAT	CAACTGGC	AGGATGTGGT	TACAGA	AGAGCTCTTCGCCACC	1556
Qy	859	TTT	AAACCTCAAG	TAAACAT	CTGACA	CAGATACTAGAT	TATTTGAT	TGAAGAAATTTACAGCT	918
Db	1557	TTCA	ACCTCAGG	TCACTTCAG	AAGTGGAC	ACAAGGTACTTTGAT	TGATGAT	GAATTCACCGCC	1616
Qy	919	CAG	ACTATTACA	TAAAC	ACCACCTG	AAAAATATGA	953		
Db	1617	CAG	TCCAATCA	CAATCAC	ACCCCCCAG	ACCGATATGA	1651		

RESULT 5

```

RES001.3
US-11-136-527-1823
; Sequence 1823, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1823
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1823

```

Query Match	Score	DB 11	Length
Best Local Similarity	52.8%	516.2	1617
Matches	71.7%	Pred. NO. 9.9e-133	
Conservative	14	Mismatches	247
Indels	3	Gaps	1

Qy	24	GACAAATGAATGATTTTGACTATTGAAACTACTAGGTAAAGGCCCTTTTGGBAAGTTAT	83
Db	477	GACCATGAACGAGATTGTAGTACCTGGAAGTACTCGGCAAGGGCACCTTTGGGAAAGGTGAT	536
Qy	84	TTTTGGTTCGACGAGAAGGCCAAGTGGAATAATCATATGCTATGAAGATTCTGAAGAAAGAAAGT	143
Db	537	CCTGGTGAAGGAGAAGGCCACAGGTGGTACTATGTCCATGAAGATCCTCAAGAAGAGGAGT	596

Qy	144	CATTATTGCAAAAGATGAAGTGGGACACACTCTAACTGAAAGCAGAGTAGTATTAAAGAACAC	203
Db	597	CATCGTTGCCAAGGATGAGGTGGCCACACGCCTTACTGAGAACCGGTGTCCTGCAGAACTC	656
Qy	204	TAGACATCCCTTTTAAACATCCTTTGAAATATCTCTCCAGACAAAAGACCGTTTGTGTTT	263
Db	657	TAGGCATCCCTTCCCTTACAGCCCTCAAGKACTCATTTCCAGACCACGACCGCCTCTGTT	716
Qy	264	TGTGATGGAAATATGTTAATGGGGCGAGCTGTTTTTCCATTTTGTTCGAGAGAGCGGTGTT	323
Db	717	TGTCATGGAGTAGCCCAATGGRGCGAGCTCTTCTTTCACCTCTCTCGTGAGCGCGTGT	776
Qy	324	CTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATGTCTCTGCGCTTGGACTATCTACA	393
Db	777	TTCAGAGGACCGGGCCGCTTCTACGGTGGGAGATTGTGTCCGCCCTGGACTACTTGCA	836
Qy	384	TTCCGGGAAAGA---TTGTGTACCGTGTATCTCAAGTTGGAGAACTTAATGCTGGACAAAGA	440
Db	837	CTCCGAGAGAACGTGGTGTACCGGACCTCAAGCTGGAGAACCTCATGCTGGACAAGGA	896
Qy	441	TGGCCACATAAAAAATTAACAGATTTTGGACTTTTCAAGAAGGGATCACAGATCAGCCAC	500
Db	897	CGGCAATCAAGATAAGGACCTTCKGGCTGTCAAGGAGGGTATCAAGSACGGTGCCAC	956
Qy	501	CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACACGAGGTGTAGAGATATGA	560
Db	957	CATGAAGACGTTCTCGGGGACACCCGAGTACCTTGGGCCMTGAGGTGCTGGAGGACACGA	1016
Qy	561	CTATGGCCGAGCAGTAGACTGTGTGGGCCCTAGGGGTGTTCATGTATGAATGATGTGTGG	620
Db	1017	CTATGGCCGTGCAGTGGACTGGTGGGGCTTGGCGGTGGTCACTGACAGATGATGTGCGG	1076
Qy	621	GAGGTACCTTTCTACACCAGGACCATGAGAAACTTTTGAATTAATATTAATGGAAGA	680
Db	1077	CCGCTGCCCTTCTACAACCAGGACCATGAGAAAGCTGTTTCGAGCTCATCTAATGAGGA	1136
Qy	681	CATTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCTTGAT	740
Db	1137	GATCCGCTTCYACGCAYACTCGGGCCGGAGGCCAAGTCCCTGCTCTCGGGGCTGCTCAA	1196
Qy	741	AAAGGATCCAAATAAACGCCCTTGGTGGAGGACAGATGATGCAAAAAGAAATATGAGACA	800
Db	1197	GAAGACCTTACACAGAGGCTCGGTGGGGCTCCGAKGACCCAWKAGATCATGACGCA	1256
Qy	801	CAGTTTCTTCTTGGAGTAAACTTGGCAAGATGATATGATAAAAAGCTTGACTCTCTT	860
Db	1257	CCGCTTCTTTGGCAACATCGTGTGGCAAGATGTTATGAGAAGAGCTGAGGCCACCTTT	1316
Qy	861	TAAACCTCAGTAACATCTGAGACAGATCTAGATATTTGTAGAGAAATTTACAGCTCA	920
Db	1317	CAAGCCCCAGGTCACTCTGAGACCCAGCACCGGTATTTTGTATGAGAGTTTACAGCTCA	1376
Qy	921	GACTATTACAATAACACCACTCGAAAAATATGA	953
Db	1377	GATGATYACCATCACRYCGCTGATYAAGATGA	1409

RESULT 6

US-10-947-249-56

; Sequence 56, Application US/10947249

; Publication No. US20050287541A1

; GENERAL INFORMATION:

; APPLICANT: AKIRA NAKAGAWARA

; APPLICANT: MIKI OHIRA

; APPLICANT: SHIN ISHII

; APPLICANT: TAKESHI GOTO

; APPLICANT: HIROYUKI KUBO

; APPLICANT: TAKAHIRO HIRATA

; APPLICANT: YASUOKA YOSHIDA

; APPLICANT: SAICHI YAMADA

; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma

; TITLE OF INVENTION: Predicting the Prognosis of Neuroblastoma

RESULT 6

```

RESULT 6
US-10-947-249-56
; Sequence 56, Application US/10947249
; Publication No. US20050287541A1
;
; GENERAL INFORMATION:
; APPLICANT: AKIRA NAKAGAWARA
; APPLICANT: MIKI OHIRA
; APPLICANT: SHIN ISHII
; APPLICANT: TAKESHI GOTO
; APPLICANT: HIROYUKI KUBO
; APPLICANT: TAKAHIRO HIRATA
; APPLICANT: YAEUKO YOSHIDA
; APPLICANT: SAICHI YAMADA
;
; TITLE OF INVENTION: Microarray for
;
; TITLE OF INVENTION: Predicting the

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; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1715
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-947-249-56

Query Match      52.7%; Score 515.8; DB 7; Length 1715;
Best Local Similarity 72.0%; Pred. No. 1.3e-132;
Matches 673; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 19 AGAAGACCAATCAATGATTTCGACTATTGAACTACTAGGTAAGGCACTTTTGGGAAA 78
DB 639 AAAGTGACCATGAATGACTTCGACTATCTCAAACTCCTTGGCAAGGAACCTTTGGCANA 698

QY 79 GTTATTTTGGTTCGAGAGAGCAAGTGGAAATACTATGTATGAAGATTCTGAAGAAA 138
DB 699 GTCATCTTGGTGGGAGAGAGCCACTGCGCTACTAGCCCATGAAGATCCTGCGAAG 758

QY 139 GAAGTCATTATGCAAGAGTGAAGTGGCAACACTCTAACTGAAAGCAGAGATTAAAG 198
DB 759 GAAGTCATTATGCAAGAGTGAAGTGGCTCACAGATCACCGAGAGCGGGTCTCCAG 818

QY 199 AACACTAGACATCCCTTTTACATCTTGAATATCTTCCACACAAAGACCGTTTG 258
DB 819 AACACAGAGCCCGTTCCTCTAGCTGGTGAAGTATGCCCTCCAGACCCAGCCGCTG 878

QY 259 TGTATTTGATGGAATATGTTAATGGGGCGAGCTGTTTTCCATTTGTCGAGAGAGCGG 318
DB 879 TGCTTTGTGATGAGTATGCCAACGGGGTGAGCTGTTCTTCCACCTGTCCCGGAGCGT 938

QY 319 GTGTTCTCTGAGGACCGCACAGTTTCTATGTGTGAGAAATTTGTCTGTCCCTTGACTAT 378
DB 939 GTCTTTCACAGAGAGCGGGCCCGGTTTTATGTGTGAGAGATTGTCTCGGCTCTTGATAC 998

QY 379 CTACATTCGGAAAGATTTGTGTACCGTGATCTCAAGTTGGAGAACTAATCTGCGACAAA 438
DB 999 TTGCACTCGCGGAGCGTGGTATACCGCGACATCAAGCTGGAAGACCTCATGTGACAAA 1058

QY 439 GATGGCCACATAAAATTTACAGATTTTGACATTTGCAAGAGAGGATCACAGATGCAGCC 498
DB 1059 GATGGCCACATCAAGTCACTGACTTTGGCTCTGCAAGAGGGCATCAGTGACCGGGGCC 1118

QY 499 ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAAGAGGTTTGAAGATAAT 558
DB 1119 ACCATGAAGAACCTTCTGTGGGACCCCGAGTAGTACCTGGCGCTGTGAGGTGCTGGAGACAAT 1178

QY 559 GACTATGGCCGAGCAGTACGCTGGTGGGCGCTAGGGGTGTCTATGTGAATGATGTGT 618
DB 1179 GACTATGGCCGCGGCGTGGACCTGTGGTGGGCGCTGGGTGTGTCTATGTGAATGATGTGT 1238

QY 619 GCGAGGTTACCTTTCTACACACGAGACCATGAGAACTTTTGAATTAATTAATGAAGAA 678
DB 1239 GCGCGCTGCCCTTTCTACACACGAGACCATGAGCGCTCTTTCGAGCTCATCTCATGGNA 1298

QY 679 GACATTAATTTCTCGAACAACCTCTCTCTCAGATGCAAAATCATTTCTTCAGGGCTCTTG 738
DB 1299 GAGATCCGCTTCCCGCGCAGCTCAGCCCCGAGGCCAAGTCCCTGCTTCTGGGCTGCTT 1358

QY 739 ATAAAGGATCCAAATAAACCCCTTGGTGGAGGACGAGATGATGCAAGAAATTAATGAGA 798
DB 1359 AAGAAGGACCCCAAGCAGAGGCTTGGTGGGCGGCCCGCAGCGATGCCAAGAGGCTCATGGAG 1418

QY 799 CACAGTTTCTCTCTCGAGCTAAACTGGCAAGATGTATATGATAAAAGCTTCTACTCTCT 858
DB 1419 CACAGTTTCTCTCTCGAGCTAACTGGCAGGACGTGGTCCAGAGAGCTCTCTGCACCC 1478

; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/11/36527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/36,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7052
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7052

Query Match      41.1%; Score 401.8; DB 11; Length 600;
Best Local Similarity 92.9%; Pred. No. 2.7e-101;
Matches 421; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 499 ACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGCACCAAGAGGTGTTGAAGATAAT 558
DB 2 ACCATGAAGACATTTCTGTGTACACAGAGTATCTGGCACCAAGAGGTATTAAGAGATAAT 61

QY 559 GACTATGGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTGTGTATGTAATGATGTGT 618
DB 62 GACTATGGCCGAGCTGTGGACTGTGGTGGGGCCCTAGGTGTGTCTATGTAATGATGTGT 121

QY 619 GGGAGTTTACCTTTCTCAACACGAGACCATGAGAACTTTTGAATTAATTAATGAGAA 678
DB 122 GGGAGTTTGCCTTTCTCAACACGAGATCATGAGAACTTTTGAATTAATTAATGAGAA 181

QY 679 GACATTAATTTCTCTCGAAGCACTCTCTTCAGATGCAAAATCATTTCTTCAGGGCTCTTG 738
DB 182 GACATCAATTTCTCTCGAAGCACTCTCTTCAGATGCAAAAGTCAATTCCTTCAGGGCTCTTG 241

QY 739 ATAAAGGATCCAAATTAACCGCTTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGA 798
DB 242 ATAAAGGATCCAAATTAACCGCTTTGGTGGAGGCGGCGAGATGATGCAAAAGAGATAATGAGG 301

QY 799 CACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTGTACTCTCT 858
DB 302 CACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTGTACTCTCTCT 361

QY 859 TTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGTGAAGAAATTTTACAGCT 918
DB 362 TTTAAGCTCAAGTAACATCTGAGACAGATACTAGATATTTTGTGAAGAAATTTTACAGCT 918

QY 919 CAGACTATTACAATAACACACCTGAAATATAT 951
DB 422 CAGACTATTACAATAACACACCTGAAATGT 454

RESULT 8
US-11-136-4033
; Sequence 4033, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

; APPLICANT: Mounts, William M									
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes									
; FILE REFERENCE: 031896-041000 (AM101086)									
; CURRENT APPLICATION NUMBER: US/11/136,527									
; CURRENT FILING DATE: 2005-05-25									
; PRIOR APPLICATION NUMBER: US 60/574,294									
; PRIOR FILING DATE: 2005-05-26									
; NUMBER OF SEQ ID NOS: 362830									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 4033									
; LENGTH: 3201									
; TYPE: DNA									
; ORGANISM: Rattus norvegicus									
US-11-136-527-4033									
Query Match 27.6%; Score 269.6; DB 11; Length 3201;									
Best Local Similarity 56.3%; Pred. No. 1.6e-64;									
Matches 525; Conservative 0; Mismatches 404; Indels 3; Gaps 1;									
Qy	20	GAAAGACAATGAATGATTTTGCATATTGGAACCTACTAGGTAAAGGCACTTTTGGGAAAG	79						
Db	1691	GGATGAAACTGACCGATTTTAACTTCCTGATGGTCTGGGAAAGGCACTTTGGCAAGG	1750						
Qy	80	TTATTTTGGTTTCGAGAGAAGCAAGTCGAAAACTACTATGCTATGAAGATTTCTGAAGAAG	139						
Db	1751	TCATGCTCTCAGAGCGGAAGGGTACAGATGAACCTCTATGCCGTGAAGATCCTGGAAGAAG	1810						
Qy	140	AAGTCATTATTGCAAGGATGAACTGGCAGACACTCTAACTGAAAGCAGAGTATTAAAGA	199						
Db	1811	ATGTGTGATCCAAGATGACGATGTGAGTGCACAATGGTGGAGAGAGGGTCTGGCCC	1870						
Qy	200	ACACTAGACATCCC---TTTTTAACATCTTTGAAATATTCCTTCCAGACAAAAGACCGTT	256						
Db	1871	TGCTGGGAAGCCCCATTCCTGACTCAGCTCCATTCCTGCTTCCAGACCATGSAACGCC	1930						
Qy	257	TGTGTTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTGTCGAGAGAGC	316						
Db	1931	TCCTACTTTATGATGGAGTATGTGAACGGGGGTGACCTCATGTACACATCCAAACAAGTTG	1990						
Qy	317	GGGTGTTTCTCTGAGGACCGCACAGTTTCTATGGTGCAGAAATTTGCTCTGCGCTTGGACT	376						
Db	1991	GCGGTTTCAAGGAGCCCATCTGCTGTAATTTACGCTGCAGAGATTTGCCATCGTCTTTTCT	2050						
Qy	377	ATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTTGGGAAATCTAATGCTGGACA	436						
Db	2051	TCITTGCAGAGCAAGGCGATCATTTACCGTGACCTGAAACTTGACAACTGATCTGGATT	2110						
Qy	437	AAGATGCCACATAAAATTTACAGATTTTGACCTTTTGCAAAGAAGGATCACAGATCGAG	496						
Db	2111	CCGAGGGGCACATCAAAATCGCTGACTTTTGGCATGTGTAAAGAGAAATCTCTGGGATGGG	2170						
Qy	497	CCACATGAAGACATTCGTGGCACTCCAGAAATCTGGCACAGAGGTGTAGAAAGATA	556						
Db	2171	TGACACCAAGACATTCGTGGCACTCCAGACTACATTTGCCCCAGAGATCATTTGCTTATC	2230						
Qy	557	ATGACTATGGCCGAGCAGTACATGCTGGGGCCCTAGGGTTGTCAATGTATGAAATGATGT	616						
Db	2231	AGCCCTACGGGAAGTCTGTGCACTGTGGCGTTTGGAGTCTCTGCTGATGAAATGTGG	2290						
Qy	617	GTGGGAGGTTACCTTTCTACAAACAGGACCATGAGAAACCTTTTGAATTTAATATTAAATGG	676						
Db	2291	CTGGCCAGGCACCTTTTGAAGGGGAGGATGAGGATGAACTCTTCCAGTCAATCATGGAGC	2350						
Qy	677	AAGACATTAAATTTCCCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTCAGGGCTCT	736						
Db	2351	ACAACTGGCGTATPCCCAAGTCCATGTCTAAGGAAAGCTGTGGCAATCTGCAAAAGGGCTAA	2410						
Qy	737	TGATAAAGGATCCAAAATAAACGCCCTTGGTGGAGGACAGATGATGCAAAAGAAATATGA	796						
Db	2411	TGACCAACACCCAGGCAGGCCCTTGGTTGTGGGCTTGAAGGGGAACGAGACATTAAGG	2470						
Qy	797	GACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATATAAAAGCTTGTACCTC	856						

Db	2471	AGCATGCATTTTCCGGTATATCGACTGGAGAAACCTCGAACCGAAGGAGATTGACCCAC	2539
Qy	857	CTTTTAAACCTCAAGTAACAATCTGAGACAGATACTAGATATTTTGTATGAAGAATTTACAG	916
Db	2531	CTTTATAAACCAAAAGCTAGAGAACGAGACACCTCCAACTTCGACAAAGAGTTTACCA	2590
Qy	917	CTCAGACTATTACAATAACACCACTGTGAAAAA	948
Db	2591	GGCAGCGCTGGTGAACCTGACTCCCACTGACAAA	2622
RESULT 9			
US-10-821-234-306/c			
; Sequence 306, Application US/10821234			
; Publication No. US20050255114A1			
GENERAL INFORMATION:			
; APPLICANT: Labat, Ivan			
; APPLICANT: Stache-Crain, Birgit			
; APPLICANT: Andarmani, Susan			
; APPLICANT: Tang, Y. Tom			
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia			
; FILE REFERENCE: 821A			
; CURRENT APPLICATION NUMBER: US/10/821,234			
; CURRENT FILING DATE: 2004-04-07			
; PRIOR APPLICATION NUMBER: US 60/462,047			
; PRIOR FILING DATE: 2003-04-07			
; NUMBER OF SEQ ID NOS: 1704			
; SOFTWARE: pt_seq_genes Version 1.0			
; SEQ ID NO 306			
; LENGTH: 3206			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-821-234-306			
Query Match 26.5%; Score 258.8; DB 7; Length 3206;			
Best Local Similarity 57.0%; Pred. No. 1.5e-61;			
Matches 514; Conservative 0; Mismatches 382; Indels 6; Gaps 2;			
Qy	33	TGATTTTGACTATTGAAACTACTAGTAAAGGCACCTTTTGGGAAAAGTTATTTTGGTTCCG	92
Db	2036	TGACTTTCACCTCTTGNAGTGATCGGAAGGGCAGTTTGGAAAGGTTCTTCTAGCAAG	1977
Qy	93	AGAGAAGGCAAGTGGAAAAATCTATGCTATGAAGATTCTGAAGAAAGAAAGTCATTTATTCG	152
Db	1976	ACACAGGCGAAGAAGTGTTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCCTGAA	1917
Qy	153	AAAGGTAGAGTGGCACACACTCTAAGTGAAGCAGAG---TATTAAAGAACACTAGACA	209
Db	1916	AAAGAAAGAGGAGGAAGCATATTATGTCGAGCGGAATGTTCTGTTGAAGAAATGTGAAGCA	1857
Qy	210	TCCCTTTTAAATCTCTTGAATAATTCCTTCCAGACAAAGACCGTTGTGTTTGTGTGAT	269
Db	1856	CCCTTTCTGGTGGGCTTCACTTCTCTTCCAGACTGCTGACAAATTTGATTTGTCTCT	1797
Qy	270	GGAAATATGTTAAATGGGGGCGAGCTGTTTTTCCATTTGTTCGAGAGAGCGGGTGTCTCTGA	329
Db	1796	AGACTACATTAATGGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTCTGGA	1737
Qy	330	GGACCGCACAGCTTTCTATGGTCAGAAATTTGTTCTGCGCTTGGCACTCTACATTCGGG	389
Db	1736	ACCACGGGCTCGTTTCTATGCTGCTGAAATAGCCAGTGGCTTGGGCTTACCTGCAATTCAC	1677
Qy	390	AAAGATTGTCTACCGTGATCTCAAGTTGGAGAAATCTAATCTCGACAAAAGATGGCCACAT	449
Db	1676	GAACATCGTTTATAGAGACTTAAACAGAGAAATATTTTCTAGATTTCAGGGACACAT	1617
Qy	450	AAAAATPACAGATTTTGGACTTTTGCAAAGAAAGGGATCACAGATGCAGCCACCATGAAGAC	509
Db	1616	TGTCCTTACTGACTTGGACTCTGCAAGGAGAACTTTGAACACAAACAGCACCAATCCAC	1557
Qy	510	ATTCTGTGGCACTTCAGAAATATCTGGCACAGAGGTGTTAGAGATTAATGACTATTGGCCG	569
Db	1556	CTTCTGTGGACGCGCGAGATCTTCGCACCTGAGTGTCTTATGAAGCAGCCTTATGACAG	1497

QY 570 AGCAGTAGACTGGTGGGCTAGGGTCTCATGTATGAATGATGTGTGGAGGTTACC 629
Db 1496 GACTGTGGAGCTGGTGGCTGGGAGCTGTCTGTATGAGATGCTGTATGGGCTGCCGCC 1437
QY 630 TTTCTACACACAGGACCATGAGAACTTTTGAATTAATTAATTAATGAAGACATTAAT 689
Db 1436 TTTTATAGCCGAAACACAGCTGAATGTACGACAACTTCTGAACAGCCTCTCCAGCT 1377
QY 690 TCCTGAACACTCTCTTTCAGATGCAAAATCATTTGCTTTTCAGGCTCTTGTATGAAGATCC 749
Db 1376 GAAACCAATATTAACAATTCGCAAGACACCTCTCGAGGGCTCTGCGAAGAGCAG 1317
QY 750 AAATAAACCCCTTGGTGGAGCCAGCATGATGCAAAAGAAATATGAGACACAGTTTCTT 809
Db 1316 GACAAAGCGGCT--CGGGGCCAAGGATGACTTCATGGGAGATTAAAGAGTCATGTCTTCTT 1260
QY 810 CTCCTGAGTAACCTGCGAAGATGTATATGATAAAAGCTTTGTACCTCTTTTAAACCTCA 869
Db 1259 CTCCTTAATTAAGGATGATCTCATTAATTAAGAGATTACTCCCTTTTAAACCCAA 1200
QY 870 AGTAACATCTGAGACAGATPACTAGATATTTTGTATGAAGAAATTTACAGCTCAGACTATTAC 929
Db 1199 TGTGAGTGGGCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTGCC 1140
QY 930 AA 931
Db 1139 CA 1138

RESULT 10

US-11-136-527-2486
; Sequence 2486, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2486
; LENGTH: 2453
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2486

Query Match 25.9%; Score 253.6; DB 11; Length 2453;
Best Local Similarity 57.5%; Pred. No. 3.8e-60;
Matches 514; Conservative 1; Mismatches 370; Indels 9; Gaps 3;
QY 33 TGATTTTGACTATTGAACTACTAGGTAAGGCACTTTTGGAAAGTTATTGTTGGTCG 92
Db 353 TGACTTCCACTCTTGGAAAGTGATCGAAAGGCGAGTTTGGAAAGTTCTTCTAGCAAG 412
QY 93 AGAAGAGGCAAGTGGAAATATCTATGCTATGAAGTCTGAAGAAAGAGTCATTATTGC 152
Db 413 GCACAGGCGAAGAGCAATCTATGCCGCTCAAGTTTGGCAGAAAGAACCTCTTGA 472
QY 153 AAAGATGAAGTGGGACACACTCTAACTGAAAGCAGAG--TATTAAGAACACTAGACA 209
Db 473 GAAGAAGGAGGAGGAGCATATTATGTCAGAGCGCATGTCTGTGAAGATGTGAAGCA 532
QY 210 TCCCTTTTAAATCTTGAATATTCTTTCAGACAAAGACCGTTGTGTTTGTGAT 269
Db 533 CCCTTTCCCTGGTGGGCTTCACTTCTCTTTCAGACTGTGACAAACTCTACTCTGCTCT 592
QY 270 GGAATATGTTAATGGGGCGAGCTGTTTTCATTTGTGAGAGAGCGGTTCTCTGA 329

Db 593 AGACTACATTAAATGGGAGAGCTGTTTCTACCATCTCCAGAGGAGCGCTGTTCTCTGA 652
QY 330 GGACCGCACACGTTTCTATGTGCGAATAATGTCTCTGCTTGGACTATCTACATTCGG 389
Db 653 ACCCGTCTCGCTCTACGCGAGCTGAAATAGCCAGTGCCTTGGGTATCTGCACTCCCT 712
QY 390 AAGATTTGTGTACCTGTATCTCAAGTTGGAGNACTTAATGCTGGCAAGATGCGGCACAT 449
Db 713 AAACATCGTTTATCGAGACTTAAACCCAGAGAATATTCTCTTAGACTCACAGGACACAT 772
QY 450 AAAAATTAACAGATTTTGACTTTTGCAAAAGAGGATCACAGATGCGCCACCACCATGAAGAC 509
Db 773 CGTCTCTACTGACTTTTGGCTCTGCAAGAGAAACATCGACACATGGGACAACTGCCAC 832
QY 510 ATTCTGTGGCACTCCAGAAATATCTGGCACCAAGAGGTGTGAAGATAATGACTATGGCG 569
Db 833 CTTCTGTGGCACGCTGAGTATCTGCTCTGAGGTCTCCATAAGACGAGCCGTACGACCG 892
QY 570 AGCAGTAGACTGGGCGCTAGGGTGTCTATGATGAATGATGTGTGGAGGTTACC 629
Db 893 GACAGTGGACTGGTGGTGGCTCGGGGCTGTCTTGTATGAGATGCTCTATGGCCTGCCTCC 952
QY 630 TTTCTACAAACAGGACCATGAGAACTTTTGAATTAATTAATTAATGAAGACATTAAT 689
Db 953 GTTCTACAGCGGGAACACAGCGGAGATGTATGA---CAATATCTGAACAGCCTCTCCA 1009
QY 690 TCCTCGAAACACTCTCTTCAGATGCAAAATCATTTGCTTTTTCAGGGCTCTTGTATGAAGATCC 749
Db 1010 GCTGAAATAATATCAACCACTCAGCAAGGCACCTGCTGGAGGCGCTCTGCAAGAGGACCG 1069
QY 750 AAATAAACGCTTGTGGAGGACGATGATGCAAAAGAAATTAATGAGACAGTTTCTT 809
Db 1070 GACCAAGAGGCTGGGT---GCCAAGGATGACTTTTATGAGATTAAGAGTCATATTTCTT 1126
QY 810 CTCCTGAGTAAACTGGCAAGATGTATATGATAAAAGCTTTGTACCTCTTTTAAACCTCA 869
Db 1127 STCTTTGATTAAGTGGGATGATCTCATTAATAAGAGATCACGCCCCCATTTTAAACCCAA 1186
QY 870 AGTAACATCTGAGACAGATCTAGATATTTTGTATGAAGAAATTTACAGCTCAGAC 923
Db 1187 TGTGAGCGGGCCAGTGAACCTTGGCACTTTTGTATCCGAGTTTACTCTGAGAGGCC 1240

RESULT 11

US-11-000-688-1184
; Sequence 1184, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000,688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1184
; LENGTH: 3017
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3017)
; OTHER INFORMATION: protein kinase c, beta 1(PRKCB1) gene.
US-11-000-688-1184

Query Match 25.2%; Score 246.4; DB 11; Length 3017;
Best Local Similarity 55.6%; Pred. No. 4e-58;

Matches 516; Conservative 0; Mismatches 406; Indels 6; Gaps 2;	
Qy 20	GAAGACAAATGATTTTACATTTTGAACCTAGGTAAAGGACATTTTGGGAAG 79
Db 1164	GGATGAACACTACCGATTTTAACTTCCATAATGGTCTGGGAAAGGACGCTTTGGCAAGG 1223
Qy 80	TTATTTTGGTTTCGAGAGAACCAAGTGGAAATATCTATGCTATGAAGATCTGAAGAAG 139
Db 1224	TCATGCTTTAGAACGAAAGGACAGATGAGCTATGCTGTGAAGATCTGAAGAAGG 1293
Qy 140	AAGTCATTTGCAAGAGATGAAGTGGCACACACTCTAACTGAAGAGCAGAGATTAAGA 199
Db 1284	ACGTTGTGATCAAGATGATACGCTGGAGTGCATATGCTGGAGAAGCGGCTGTGGCCC 1343
Qy 200	ACACT---AGACATCCCTTTTAAACATCTTGAATATTCCTCCAGACAAAGACGTT 256
Db 1344	TGCTGGGAGCCGCTTCTGACCCAGCTCCACTCTGCTTCCAGACCAATGAGCCGCC 1403
Qy 257	TGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTTGTGAGAGAGC 316
Db 1404	TGTACTTTGTGATGGAGTACGTGAATGGGGCGACCTCATGTATCACATCCAGCAAGTCG 1463
Qy 317	GGGTGTTCTCTGAGGACCGGACACAGTTTCTATGTGTGAGAAATTTGCTGCTCCCTGGACT 376
Db 1464	GCCGGTTCAAGGAGCCCATGCTGTATTTTACGCTGCAGAAATTCCTATCGTCTGTCT 1523
Qy 377	ATCTACATTCGGAAAGATTGCTACCGTGATCTCAAGTTGGAGATCTAATGCTGGACA 436
Db 1524	TCTTACAGAGTAAGGCAATTTTACCGTGACCTTAAACCTTGACACGATGATGCTCGATT 1593
Qy 437	AAGATGGCCACATAAAATTAACAGATTTTGGACTTTGCAAGAGAGGGATCACAGATCGAG 496
Db 1584	CTGAGGGACACATCAAGATTGCCGATTTTGGCATGTGTAGGAAACATCTGGGATGGG 1643
Qy 497	CCACATGAAGACATTTCTGGGCACTCCAGAAATATCTGGGACACAGAGGTGTGAAGATA 556
Db 1644	TGACAAACCAAGACATTTCTGGGCACTCCAGACTACATCGCCCCGAGATAATTCCTTATC 1703
Qy 557	ATGACTATGGCGAGCAGTACGCTGGGGCCTAGGGGTTGTCATGTATGAATATGAT 616
Db 1704	AGCCCTATGGGAAGTCCGTGGATTTGGTGGCAATTTGGAGTCTCTGTATGAATATGTTG 1763
Qy 617	GTGGGAGGTTACCTTTCTACAAACAGGACCAATGAGAACTTTTGAATTAATTAATGG 676
Db 1764	CTGGGAGGACACCTTTTGAAGGGGAGATGAAGTGAATCTTCCATCCATCAATGGAAC 1823
Qy 677	AAGACATTAATTTCTCGAACAACCTCTCTTCAGATGCAAAATCATTTGCTTTCAGGGCTCT 736
Db 1824	ACAAAGTAGCCTATCCCAAGTCTATGTCGAAGGAGCTGTGGCCATCTGCAAGGGCTGA 1883
Qy 737	TGATAAAGGATCCAAATAAACGCTTGGTGAGGACCAAGATGATGCAAAAGAAATTA 796
Db 1884	TGACCAAAACCCAGGCAACGCTGGGTTGTGGACCTTGAAGGCGAAGCGTATATCAAG 1943
Qy 797	GACACAGTTCTTCTCTGGAGTAACTGGCAAGATGTATATGATAAAAGCTTTTACCTC 856
Db 1944	AGCATGCATTTTCCGGTATATGATTTGGGAGAACTTGAACGCAAGAGATCCAGCCCC 2003
Qy 857	CTTTTAAACCTCAAGTAACTCTGAGACAGATATCTAGATATTTTGTATGAAGATTTACAG 916
Db 2004	CTTATAAGCCAAAAG---CTTGTGGCGAATGCTGAAAACTTCGACCGATTTTTCACCC 2060
Qy 917	CTCAGACTATTACAATACACCACTGA 944
Db 2061	GCCATCCACCAAGTCTTAACACCTCCCGA 2088

RESULT 12
US-11-136-527-2878
; Sequence 2878, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William M	
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes	
; FILE REFERENCE: 031896-041000 (AM101086)	
; CURRENT APPLICATION NUMBER: US/11/136,527	
; CURRENT FILING DATE: 2005-05-25	
; PRIOR APPLICATION NUMBER: US 60/574,294	
; PRIOR FILING DATE: 2005-05-26	
; NUMBER OF SEQ ID NOS: 362830	
; SOFTWARE: PatentIn version 3.2	
; SEQ ID NO 2878	
; LENGTH: 2615	
; TYPE: DNA	
; ORGANISM: Rattus norvegicus	
US-11-136-527-2878	
Query Match 24.28; Score 236.4; DB 11; Length 2615;	
Best Local Similarity 55.6%; Pred. No. 2.2e-55;	
Matches 497; Conservative 0; Mismatches 391; Indels 6; Gaps 2;	
Qy 28	ATGAATGATTTTGACTATTTTGAACACTACTAGGTAAAGGCACCTTTTGGGAAAGTTATTG 87
Db 1082	ATCGACAACCTTTGAGTTTCATCCGGGTGTTGGGNAAGGGAGCTTCGGGNAAGTGTATGCTC 1141
Qy 88	GTTGAGAGAGGCAAGTGGAAAATACTATGCTATGAAGATTCTGAAGAAGAAAGTCAAT 147
Db 1142	GCCAGATAAAGGAGACAGGAGAGCTGTACGCTGTGAAGGTGCTGAAGAGGACGTCAATC 1201
Qy 148	ATTGCAAGAGATGAAGTGGCACACACTCTAACTG---AAAGCAGAGATTATTAAGAACT 204
Db 1202	CTCAGGATGACGATGTGGAATGCACATGACTGAGAAGAGATCCCTCTCTCTGGCCCGC 1261
Qy 205	AGACATCCCTTTTAAACATCCTTGAAATATTCCTTCCAGACAAAGACCGTTTGTGTTTT 264
Db 1262	AACACCCCTTCTCACCCAGCTCTTCTGCTGCTTTTCAGACTCTCTGACCGTCTGTTCTT 1321
Qy 265	GTGATGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTTGTGAGAGAGCGGTTGTC 324
Db 1322	GTATGAGTGTGTGAACGGAGGTGACCTGATGTTTCCACATCCAAAAGTCCAGGCGTTTC 1381
Qy 325	TCGTGAGACCGCACACGTTTCTATGTTGTCAGAAATTTGCTCTGCGCTTGGACTATCTACAT 384
Db 1382	GATGAAGCCCGAGCTCGTTTTCTACGCTGCAGAGATCAATTTCTGCACATCATGTTCTCCAC 1441
Qy 385	TCGGAAAGATTTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGACAAAGATGGC 444
Db 1442	GAGAAAGGCATCATCTACAGAGACTTGAACACTGGACAAACGTAATACTTGGACCAAGAGGC 1501
Qy 445	CACATAAAAAATTACAGATTTTGGACTTTGCAAGAAAGGGATCAAGATGACAGCCACCATG 504
Db 1502	CACGTAACTGGCCGACTTCGGAAATGTCAAGAGGGGCAATTTGTAACGGGGTCAACACA 1561
Qy 505	AAGACATTTCTGGCACTCCAGATATCTGGCACCAGAGGTGTAGAAAGATAAGTACTAT 564
Db 1562	GCCACCTTTGCGGCACGCTGACTACATTTGCCCCAGAGATCCCTTCAGGAGATGTTGAT 1621
Qy 565	GGCCGACAGTAGACTGCTGGGGCTAGGGGTGCTCATGTATGAAATGATGTGTGGGAGG 624
Db 1622	GGACCTGCAGTAGACTGCTGGGCCATGGGCGTGTGCTTTATGAGATGCTGTGGGACAT 1681
Qy 625	TTACCTTTTACAAACAGGACCAATGAGAACTTTTGTAAATTAATTAATGAAGAGACAT 684
Db 1682	GCGCCCTTCAGGCGTGAGATGAAGATGACCTTTTGGAGGCCATCTGAAATGATGAAGTT 1741
Qy 685	AAATTTCTCGAACACTCTCTCAGATGCAAAATCATTTGTTTCAGGGCTCTTCATAAAG 744
Db 1742	GTCTACCTTACCTGGCTCCATGAAGATGCCACAGGGATTCCTCAAAATCTTTCATACCAAG 1801
Qy 745	GATCCAAATAAAGCGCTTGGTGG---AGGACCAAGATGATCAAAAGAAATTAATGAGACAC 801
Db 1802	AAACCCACCATGGCTTGGGACGCTGACTCAGGAGGCGGACGATGAGATCTTGAGACAT 1861
Qy 802	AGTTTCTCTCGAGTAAACTGCGCAAGATGTATATGATAAAAGCTTGTACCTCTCTTTT 861

Db 1862 CCTTCTTTAAGGAATCGACTGGTCCAGTTGAACCATGCCAGCTAGAACCCGCTTTC 1921
Qy 862 AAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGATGAAGATTTTACA 915
Db 1922 CGACCCAGAATCAAAATCCGAGAACGCTCAGCAATTTTGACCCAGACTTCATA 1975
RESULT 13
US-11-152-366-2
; Sequence 2, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 5537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-152-366-2
Query Match 23.5%; Score 229.8; DB 11; Length 5537;
Best Local Similarity 55.2%; Pred. No. 1.9e-53;
Matches 494; Conservative 0; Mismatches 392; Indels 9; Gaps 2;
Qy 29 TGAATGATTTTCACTATTGAAACTACTAGGTAAAGGCACCTTTTCGGAAGTTATTTTGG 88
Db 1411 TGGATGAGTTCACTTCACTCAAGGTGTGGGCAAGGACGCTTGGCAAGTCACTGTTGG 1470
Qy 89 TTCGAGAGAAGCAAGTGGAAATATCTATGCTATGAAGATCTCGAAGAAAGAGTCAATTA 148
Db 1471 CAGNACTCAAGGGCAAGATGAAGTATATGCTGTGAAGTCTTAAAGAAAGGACGTCATCC 1530
Qy 149 TTGCAAGATGAAGTGGACACACTCTAACTGAAGACAGATATT---AAAGAACACTA 205
Db 1531 TTCAGGATGATGACGTGGACTGCACAAATGACAGAGAAGAGGATTTTGGCTCTGGCACCGA 1590
Qy 206 GACATCCCTTTTAAACATCTCTTGAATATTCCTTCCAGACAAAGACGTTTGTGTTTG 265
Db 1591 AACACCGGTACCTTACCNACTCTACTGCTGCTTCCAGAACAGGACCGCTCTTTTTCG 1650
Qy 266 TGATGGAATATGTTAATGGGGCGAGCTGTGTTTTCCATTTTTCGAGAGCGGGTGTCT 325
Db 1651 TCATGGAATATGTAATGGTGGAGACCTCATGTTTCAGATTCAGCGCTCCCGAAATTCG 1710
Qy 326 CTGAGAACCGACACAGTTTCTATGTTGCGAGAAATTTGCTCTGCCCTTGGACTATCTACATT 385
Db 1711 ACAGAGCTCGTTTACGGTTTCTATGCTGCAGAGGTCACATCGCCCTCATGTTCTCCACC 1770
Qy 386 CCGGAAGATTTGTTACCGTGTATCTCAAGTTCGAGATCTAATGCTGGACAAAGATGGCC 445
Db 1771 AGCATGGAGTCACTACAGGGATTTGAAACTGGACAACTATCTTCTGATGCGAAGGTC 1830
Qy 446 ACATAAAATATACAGATTTTGGACTTTTGCAAGAAAGGATTCAGATGCGAGCCACCATGA 505
Db 1831 ACTGCAAGCTGGCTGACTTCGGGATGTGCAAGGAAGGATTCGATGTTGTCAGACCA 1890
Qy 506 AGACATTTCTGTGGCACTCCAGAAATATCTGGCAACGAGGTGTAGAAGATAATGACTATG 565
Db 1891 CCACGTTCTGTGGGACTCTCTGACTACATAGCTCTGAGATCTCGAGAGGATTTGGAGTATG 1950
Qy 566 GCCGAGCACTAGCTGTGGGGCTAGGGGTTGTCATGTATCAATGATGTGTGGAGGT 625
Db 1951 GCCCCCTCCGTGGACTGGTGGGGCTTGGGGTGTGATGTACGAGATGATGGCTGGACAGC 2010

Qy 626 TACCTTTCTACAAACAGGACCATGAGAAACTTTTGTGAATTAATATTAATGGAAGACATTA 685
Db 2011 CTCCTTTTGGCGCGCAAAATGAGGACGACCTATTTTGAGTCCATCTCCATGACGACGTGC 2070
Qy 686 AATTTCTCGAACACACTCTCTTTAGATGCANAATCATTCGTTTTCAGGGCTCTTGATAAAGG 745
Db 2071 TGTACCCAGTCTGGCTCAGCAAGAGGCTGTGAGCATCTTGAAGCTTTTCATGAGCAAGA 2130
Qy 746 ATCCAAATAAAGCGCTTGGTGGAGGACCA-----GATGATGCAAAAGAAATTAATGAGAC 799
Db 2131 ATCCCCCAAGCGCTGGGCTGTGTGGCATCGCAGATGGCGAGGACGCCATCAAGCAGC 2190
Qy 800 ACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAGAGCTTGTACTCTCTT 859
Db 2191 ACCCATTTCTTCAAGAGATTCAGCTGGGTGCTCTCGAGCAGAGAAGATCAAGCCACCT 2250
Qy 860 TTAACCTCAAGTAACATCTCGAGACAGATCTAGATATATTTGATGAAGAATTTAC 914
Db 2251 TCAACCAAGCATTTAAACCAAAAGAGACGTCATAATTTTGAACCAAGACTTTAC 2305
RESULT 14
US-11-136-527-1950
; Sequence 1950, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1950
; LENGTH: 3075
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1950
Query Match 23.5%; Score 229.4; DB 11; Length 3075;
Best Local Similarity 55.1%; Pred. No. 2e-53;
Matches 493; Conservative 1; Mismatches 392; Indels 9; Gaps 2;
Qy 29 TGAATGATTTTGAATTTGAACTACTAGTAAAGGCACCTTTTCGGAAGTTATTTTGG 88
Db 1407 TGGATGAGTTCAACTTCATCAAGGTGTAGGCAAAAGGACGCTTTGGCAAGTCACTGCTGG 1466
Qy 89 TTCGAGAGAAGCAAGTGGAAAATACTATGCTATGAAGATTTCTGAAGAAAGAGTCAATTA 148
Db 1467 CCGAGCTCAAGGGTAAGGATGAAGTCTATGCTGTGAAGTCTTAAAGAAAGGACGTCATCC 1526
Qy 149 TTGCAAGAGATGAAGTGGCAACACTCTAACTGAAGACAGAGTATT---AAAGAACACTA 205
Db 1527 TGCAGGATGACACGCTGGAGTGCAGATGACAGAGAAGAGGATTTTGGCTCTGGCGCGGA 1586
Qy 206 GACATCCCTTTTAACTATCTTGAATATTCCTTCCAGACAAAGACGTTTGTGTTTG 265
Db 1587 AACACCTTATCTAACCCCACTCTATTGCTGCTTCCAGACCAAGGACCGSCTCTTCTTCG 1646
Qy 266 TGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTTGTGCGAGAGCGGGTGTCT 325
Db 1647 TCATGGAATATGTAACCGTGGAGACCTCATGTTCCAGATTCAGCGGTCGCCGAAATTCG 1706
Qy 326 CTGAGAACCGCACAGTTTCTATGTTGCGAGAAATTTGCTCTGCCCTTGGACTATCTACATT 385
Db 1707 ATGAGCCTCGTTCCGGGTTCTATGCTGCCGAGGTCAACATCTGCTCTCATGTTTCTCCACC 1766
Qy 386 CCGGAAGATTTGTTACCGTGTATCTCAAGTTGGAGAACTAATGCTGGCAAGAGATGGCC 445

Db 1767 AACATGGAGTGATCTACAGGAGATTGAAACTGGACAAACATCTCTTAGATGACAGAGGTC 1826
Qy 446 ACATAAAATTTACAGATTTTGGACTTTTGCAAAGAGGATCACAGATGACAGCCACCATTGA 505
Db 1827 ACTSCAAGCTGGCTGACTTTTGGGATGTGCAAGGAAGGATTTCTGAATGGCGTGACAACTA 1886
Qy 506 AGACATTTCTGGGCACCTCCAGAAATATCTGGCACAGAGGTGTTAGAAGATAATGACTATG 565
Db 1887 CCACCTTCTGTGGGACTCTCTGACTACATAGTCTCCAGAGATCCTGACAGAGTTGGAGTAGC 1946
Qy 566 GCCGAGCAGTAGACTGTGGGGCTAGGGGTGTCATGTATGAATATGATGTGGGAGGT 625
Db 1947 GCCCCTCAGTGGACTGTGGGCCCTCGGCGTGTCTGATGTACGAGATGATGGCCGGGAGC 2006
Qy 626 TACCTTTCTACAACAGCAGCAGCAGCAAACTTTTGAATTAATTAATGAAGACATTA 685
Db 2007 CCCCTTTGAAGCTGACACAGAGACGACTTTGTTGAAATCCATCTTCAAGATGACGTTT 2066
Qy 686 AATTTCCTCGAACACTCTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTCTTTGATAAAGG 745
Db 2067 TCTACCTGTCTGGCTTAGCAAGAGGCTGTGACATCTCTGAAAGCTTTTCATGACCAAGA 2126
Qy 746 ATCCAAATAAAGCGCTTGG-----TGGAGACAGAGATGACGAAAGAAATATGAGAC 799
Db 2127 ACCCGCAAGCGCTTGGGCTGCGTGGCAGCACAGAACGGGAAAGATGCCATCAAGCAAC 2186
Qy 800 ACAGTTTCTCTCTGGAGTAACTGGCAAGATGTATATGATAAAAGCTTTGTACCTCCTT 859
Db 2187 ATCCATTTCTCAAGAGATTGACTTGGGTACTGTCTGGAGCAGAGAAATGAGCCCCCT 2246
Qy 860 TTAACCTCAAGTAACATCTGAGACAGATACATAGATATTTTGTGAAGAAATTTAC 914
Db 2247 TCAAGCCGAGAATTTAAACCAAGAGAGATGTCAATACTTTGACCAAGACTTTTAC 2301

RESULT 15

US-10-955-054A-34
; Sequence 34, Application US/10955054A
; Publication No. US2005026420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 2146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-34

Query Match 23.1%; Score 226.4; DB 7; Length 2146;
Best Local Similarity 55.1%; Pred. No. 1.2e-52;
Matches 487; Conservative 0; Mismatches 391; Indels 6; Gaps 2;
Qy 34 GATTTTGACTATTTTGAAGCTACTAGGTAAAGGCACTTTTGGGAAAGTTATTTTGGTTCGA 93
Db 499 GACTTCGACTTCCTCAAGTCATCGGCNAAAGGGAAGTACGGGAAGGTCTTACTGGCCCAAG 558
Qy 94 GAGAAGCAAGTGGAATAATCTATGCTATGAAGATTCGAAAGAAAGATCATTTATGCA 153
Db 559 CGCAAGTCTGATGGGGGTTCTATGCAAGTGAAGGTACTACAGAAAAAAGTCCATCTTAAAG 618
Qy 154 AAGCATGAGTGGGACACACTCTAACTGAAGAGCAGATATTA---AAGACACTAGACAT 210
Db 619 AAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAAAGCTGCGGCAC 678

Qy 211 CCCTTTTAAACATCTCTTGAATAATCTCTCCAGACAAAGACCGTTTGTGTGTGTGATG 270
Db 679 CCCTTCTCGTGGGCTCGCTACTCTCTCCAGACACCTGAGAAGCTCTACTTCGTGCTC 738
Qy 271 GAATATGTTAATGGGGCGAGCTGTTTTCATTTTGTGAGAGAGCGGGTGTCTCTGAG 330
Db 739 GACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGACGCGGAGCGCCGTTCTCTGGAG 798
Qy 331 GACCGCACAGTTTCTATGTGTCAGAAATGTCTGCGCTTGGACTATCTACATTTCCGGA 390
Db 799 CCCGGGCCAGGTTTCTACGCTGTGAGGTGCGCAGCGCAATGGCTACCTGCACTCCCTC 858
Qy 391 AAGATTGTGTACCGTGTATCTCAAGTTTGGAGAACTTAATGCTGGACAAAGATGGCCACATA 450
Db 859 AACATCATTTTACAGGGATCTGAAACACAGAGAACATCTCTTTGGACTGCCAGGACACGTG 918
Qy 451 AAAATTACAGATTTTGGACHTTGCAAAAGAGGAGTACAGATGCGAGCCACCATGAAGACA 510
Db 919 GTGCTGACGGAATTTTGGCCCTCTCAAGGAAGGTGTAGAGCCTGAAGACACCCACATCCACA 978
Qy 511 TTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAAGATAATGACTATGGCCGA 570
Db 979 TTCTGTGGTACCCTCTGAGTACTTGGCACCTGAAGTGTCTCGAAGAGAGCCTTATGATCGA 1038
Qy 571 GCAGTAGACTGTGTGGGCTTGTGAGGTTGTGATGATAAGATGATGTGGGAGGTTACCT 630
Db 1039 GCAGTGGACTGGTGGTGTGTTGGGGCGAGTCTCTACGAGATGCTCCATGGCTGCCGCC 1098
Qy 631 TTCTACAAACAGGACCATGAGAAACTTTTGAATTAATATTAATGGAAGACATTAATTTT 690
Db 1099 TTCTACAGCCCAAGATGTATCCAGATGTATGAGAACAATCTGCAACCAGCGCTACAGATC 1158
Qy 691 CCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCTTTGATAAAGGATCCA 750
Db 1159 CCCGAGGCCGACAGTGGCGGCTGTGACCTCTGCAAAAGCCTTCTCCACAGGACCCAG 1218
Qy 751 AATAAAAGCGCTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGACACAGTTTCTTC 810
Db 1219 AGGCAGCGGCTGGGCTCCAAAGCAGACTTT---CTTGAGATTAAAGAACCATGTATTCTTC 1275
Qy 811 TCTGGAGTAACTGGCAAGATGTATGATAAAAGCTTGTACCTCTCTTTTAAACCTCAA 870
Db 1276 AGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCTTTCAACCCAAAT 1335
Qy 871 GTAACATCTGAGACAGATACATAGATATTTTGTGAAGAAATTTAC 914
Db 1336 GTGACAGGACCTGCTGACTTGAAGCATTTTGAAGGAGTTTAC 1379

Search completed: February 15, 2006, 06:57:30
Job time : 260 secs

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 05:54:12 ; Search time 858 Seconds
(without alignments)
9425.934 Million cell updates/sec

Title: US-10-601-311-2

Perfect score: 978
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	2811	6	US-10-324-985A-4
2	978	100.0	2811	8	US-10-753-267-107
3	949.8	97.1	1570	3	US-09-526-043-1
4	949.8	97.1	1570	6	US-10-394-568-1
5	949.8	97.1	1570	10	US-11-063-691-1
6	949.8	97.1	1703	9	US-10-887-553A-692
7	689	70.4	2410	3	US-09-771-161A-66
8	527	53.9	1722	7	US-10-322-281-412
9	527	53.9	1741	6	US-10-324-985A-2
10	527	53.9	1741	8	US-10-735-461-21
11	527	53.9	3010	9	US-10-895-225A-57
12	525	53.7	1140	6	US-10-324-985A-5
13	525	53.7	1443	10	US-11-166-990-66
14	525	53.7	2626	7	US-10-324-985A-1
15	525	53.7	2626	7	US-10-713-678-5
16	525	53.7	2626	8	US-10-735-461-20
17	525	53.7	2626	9	US-10-895-225A-56
18	517.4	52.9	2562	7	US-10-322-281-415
19	515.8	52.7	1599	6	US-10-324-985A-3
20	515.8	52.7	1599	7	US-10-641-643-1004
21	515.8	52.7	1715	6	US-10-007-926A-254
22	515.8	52.7	1715	8	US-10-735-461-23
23	512.2	52.4	2729	9	US-10-895-225A-36

24	512.2	52.4	2978	3	US-09-955-999-43	Sequence 43, Appl
25	510.6	52.2	2181	5	US-10-072-036-70	Sequence 70, Appl
26	510.6	52.2	2184	5	US-10-072-036-138	Sequence 138, App
27	510.6	52.2	2610	3	US-09-970-000-3	Sequence 3, Appl
28	510.6	52.2	2610	6	US-10-388-263-329	Sequence 329, App
29	510.6	52.2	2610	7	US-10-641-643-1206	Sequence 1206, Ap
30	510.6	52.2	2610	7	US-10-713-678-1	Sequence 1, Appl
31	510.6	52.2	2610	8	US-10-735-461-22	Sequence 22, Appl
32	510.6	52.2	2610	9	US-10-823-433-3	Sequence 3, Appl
33	510.6	52.2	2610	9	US-10-956-157-1382	Sequence 1382, Ap
34	510.6	52.2	2707	9	US-10-956-157-4334	Sequence 4334, Ap
35	499.6	51.1	1854	5	US-10-198-846-9984	Sequence 9984, Ap
36	493	50.4	1254	7	US-10-713-678-3	Sequence 3, Appl
37	430.8	44.0	2375	10	US-11-097-143-25901	Sequence 25901, A
38	430.8	44.0	2425	10	US-11-097-143-40607	Sequence 40607, A
39	430.8	44.0	3712	8	US-10-473-939-7	Sequence 7, Appl
40	429.2	43.9	550	10	US-11-060-756-3130	Sequence 3130, Ap
41	429.2	43.9	550	10	US-11-060-756-3131	Sequence 3131, Ap
42	429.2	43.9	550	10	US-11-060-756-7402	Sequence 7402, Ap
43	429.2	43.9	550	10	US-11-060-756-7403	Sequence 7403, Ap
44	410.6	42.0	2583	9	US-10-450-763-20291	Sequence 20291, A
45	383.8	39.2	387	6	US-10-168-771-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-324-985A-4
; Sequence 4, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US1/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: human
US-10-324-985A-4

Query Match	100.0%	Score	978	DB	6	Length	2811
Best Local Similarity	100.0%	Pred. No.	7.6e-253	Mismatches	0	Indels	0
Matches	978	Conservative	0	0	0	Gaps	0
Qy	1	TCTACAA	CCCATCATATAAAGAAAGACAATGAATGATTTTGGCTATTTGAACTACTAGT	60			
Db	406	TCTACAA	CCCATCATATAAAGAAAGACAATGAATGATTTTGGCTATTTGAACTACTAGT	465			
Qy	61	AAAGCACTTTTGGGAAAGTATTTTGGTTCAGAGAGGCAAGTGGGAAATTAATGCT	120				
Db	466	AAAGCACTTTTGGGAAAGTATTTTGGTTCAGAGAGGCAAGTGGGAAATTAATGCT	525				
Qy	121	ATGAAGATTCAGAGAGAGTCAATATTCAGAGAGTGAAGTGCACACACTCTAACT	180				
Db	526	ATGAAGATTCAGAGAGAGTCAATATTCAGAGAGTGAAGTGCACACACTCTAACT	585				
Qy	181	GAAACAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC	240				
Db	586	GAAACAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC	645				
Qy	241	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTATGGGGGAGCTGTTTTTC	300				
Db	646	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTATGGGGGAGCTGTTTTTC	705				
Qy	301	CATTTGTGAGAGAGCGGTGTTCTCTGAGGACCCGACACAGTTTCTATGTCGACAGAAAT	360				

Db 706 CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCCACACGTTTCTATGGTGCAGAAATT 765
Qy 361 GTCTCTGCTTGGACTACTACATTCGGAAGAAGTTGTACCGTGTATCTCAAGTTGGAG 420
Db 766 GTCTCTGCTTGGACTACTACATTCGGAAGAAGTTGTACCGTGTATCTCAAGTTGGAG 825
Qy 421 AATCTAATGCTGGCAAAAGATGGCCACATAAAAAATTACAGATTTTGGACTTTGCAAGAA 480
Db 826 AATCTAATGCTGGCAAAAGATGGCCACATAAAAAATTACAGATTTTGGACTTTGCAAGAA 885
Qy 481 GGGATCAGATGCGAGCCACATGAAGACATCTGTGGCACTCAGAAATATCTGGCCACCA 540
Db 886 GGGATCAGATGCGAGCCACATGAAGACATCTGTGGCACTCAGAAATATCTGGCCACCA 945
Qy 541 GAGGTGTTAGAAATATGACTATGGCCGACGATAGACTGTGGGCGCTAGGGGTTGTC 600
Db 946 GAGGTGTTAGAAATATGACTATGGCCGACGATAGACTGTGGGCGCTAGGGGTTGTC 1005
Qy 601 ATGTATGAATGATGTGTGGGAGGTTACCTTTCTTCAACACGAGGACCATGAGAACTTTTT 660
Db 1006 ATGTATGAATGATGTGTGGGAGGTTACCTTTCTTCAACACGAGGACCATGAGAACTTTTT 1065
Qy 661 GAATTAATATTAATGGAAGACATTAATTTCTCTCGAACACTCTCTCAGATGCAAAATCA 720
Db 1066 GAATTAATATTAATGGAAGACATTAATTTCTCTCGAACACTCTCTCAGATGCAAAATCA 1125
Qy 721 TTGCTTTTCAGGCTCTTGATAAAGATCCAAATAAACGCCCTTGTGGAGGACACAGATGAT 780
Db 1126 TTGCTTTTCAGGCTCTTGATAAAGATCCAAATAAACGCCCTTGTGGAGGACACAGATGAT 1185
Qy 781 GCAAAAGAAATTTATGAGACACAGTTTCTCTCTGAGGTAAACTGGCAAGATGTATATGAT 840
Db 1186 GCAAAAGAAATTTATGAGACACAGTTTCTCTCTGAGGTAAACTGGCAAGATGTATATGAT 1245
Qy 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAAATCTGAGACAGATACTAGATATTTT 900
Db 1246 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAAATCTGAGACAGATACTAGATATTTT 1305
Qy 901 GATGAAGATTTTACAGCTCAGACTATTACAAATACACACCTGAAATATGATGAGGAT 960
Db 1306 GATGAAGATTTTACAGCTCAGACTATTACAAATACACACCTGAAATATGATGAGGAT 1365
Qy 961 GGTATGGACTGTCATGGAC 978
Db 1366 GGTATGGACTGTCATGGAC 1383

RESULT 2
US-10-753-267-107
; Sequence 107, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003P18NOWNIM
; CURRENT APPLICATION NUMBER: US/10753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683

; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1440)
; US-10-753-267-107

Query Match 100.0%; Score 978; DB 8; Length 2811;
Best Local Similarity 100.0%; Pred. No. 7.6e-253; Mismatches 0; Indels 0; Gaps 0;
Matches 978; Conservative 0;

Qy 1 TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACATATTTTGAACACTACTAGT 60
Db 406 TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACATATTTTGAACACTACTAGT 465
Qy 61 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 120
Db 466 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 525
Qy 121 ATGAAGATTCGAAAGAAAGAAAGTCATTATTGCAAAAGGATGAAGTGGGCACACACTCTAACT 180
Db 526 ATGAAGATTCGAAAGAAAGAAAGTCATTATTGCAAAAGGATGAAGTGGGCACACACTCTAACT 585
Qy 181 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTTTAAACATCCCTTTTTC 240
Db 586 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTTTAAACATCCCTTTTTC 645
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGGAGCTGTTTTTC 300
Db 646 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGGAGCTGTTTTTC 705
Qy 301 CATTGTGCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGCTTCTATGTCGAGAAAT 360
Db 706 CATTGTGCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGCTTCTATGTCGAGAAAT 765
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATGTGTACCGTGTATCTCAAGTTGGAG 420
Db 766 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATGTGTGTACCGTGTATCTCAAGTTGGAG 825
Qy 421 AATCTAATGCTGCAGAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAGAA 480
Db 826 AATCTAATGCTGCAGAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAGAA 885
Qy 481 GGGATCAGATGCGAGCCACCATGAAGACATCTGTGGCACTCAGAAATATCTGGCACCA 540
Db 886 GGGATCAGATGCGAGCCACCATGAAGACATCTGTGGCACTCAGAAATATCTGGCACCA 945
Qy 541 GAGGTGTTAGAAATATGACTATGCGCGACGATAGACTGTGGGCGCTAGGGGTTGTC 600

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Db 946 GAGGTGTTAGAGATAATGACTATATGGCCGAGCAGTAGACTGTGTGGGCTTAGGGGTTGTC 1005
QY 601 ATGTATGAAATGATGTGGAGGTTA CTTTCTCAACCCAGGACCATGAGAAACTTTT 660
Db 1006 ATGTATGAAATGATGTGGAGGTTACCTTTCTCAACCCAGGACCATGAGAAACTTTT 1065
QY 661 GAATTAATTAATTAATGGAACACATTAATTTCTCCGAACTCTCTTCAGATGCAAAATCA 720
Db 1066 GAATTAATTAATTAATGGAACACATTAATTTCTCCGAACTCTCTTCAGATGCAAAATCA 1125
QY 721 TTGCTTTACAGGCTCTCTGTATAAGGATCCAAATAAAACGCTTTGGTGGAGCACCATGAT 780
Db 1126 TTGCTTTACAGGCTCTCTGTATAAGGATCCAAATAAAACGCTTTGGTGGAGCACCATGAT 1185
QY 781 GCAAAAGAAATTAATGAGACACAGTTCTTCTCTGAGATGAACCTGGCAAGATGTATATGAT 840
Db 1186 GCAAAAGAAATTAATGAGACACAGTTCTTCTCTGAGATGAACCTGGCAAGATGTATATGAT 1245
QY 841 AAAAGCTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 900
Db 1246 AAAAGCTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 1305
QY 901 GATGAAGAAATTAACAGCTCAGACTATTACAATAACACCACTGAAATAATGATGAGAT 960
Db 1306 GATGAAGAAATTAACAGCTCAGACTATTACAATAACACCACTGAAATAATGATGAGAT 1365
QY 961 GGTATGGACTGCATGGAC 978
Db 1366 GGTATGGACTGCATGGAC 1383
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RESULT 3

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US-09-526-043-1
; Sequence 1, Application US/09526043
; Publication No. US20030100049A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526, 043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-09-526-043-1
```

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Query Match 97.1%; Score 949.8; DB 3; Length 1570;
Best Local Similarity 99.8%; Pred. No. 2.3e-245;
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTACAACCCATCATAAAAAGAACAAATGAATGATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGGT 60
Db 531 TCTACAACCCATCATAAAAAGAACAAATGAATGATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGGT 590
QY 61 AAAGGCATTTTGGGAAAGTATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGGT 120
Db 591 AAAGGCATTTTGGGAAAGTATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGGT 650
QY 121 ATGAAGATTCTGAAGAAAGAAAGTCATTATTGCAAAAGGATGAAGTGGCAACACTCTAACT 180
Db 651 ATGAAGATTCTGAAGAAAGAAAGTCATTATTGCAAAAGGATGAAGTGGCAACACTCTAACT 710
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QY 191 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCTTGAATATTTCCTTC 240
Db 711 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCTTGAATATTTCCTTC 770
QY 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTTC 300
Db 771 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTTC 830
QY 301 CATTTGTCGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTTCTATGGTGCAGAAATT 360
Db 831 CATTTGTCGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTTCTATGGTGCAGAAATT 890
QY 361 GTCCTGCTTTGGACTATCTACATTTCCGGAAGATGTTGTACCGTGATCTCAAGTTGGAG 420
Db 891 GTCCTGCTTTGGACTATCTACATTTCCGGAAGATGTTGTACCGTGATCTCAAGTTGGAG 950
QY 421 AATCTAATGCTGGACAAAAGATGGCCACATAAAAAATACAGATTTTGGACTTTTGCAGAA 480
Db 951 AATCTAATGCTGGACAAAAGATGGCCACATAAAAAATACAGATTTTGGACTTTTGCAGAA 1010
QY 481 GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGACCA 540
Db 1011 GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGACCA 1070
QY 541 GAGGTGTTAGAAGATAATGACTATGCGCCGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 600
Db 1071 GAGGTGTTAGAAGATAATGACTATGCGCCGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 1130
QY 601 ATGTATGAAATGATGTGTGGAGGTTTACCTTTCTACAACCCAGGACCATGAGAAACTTTT 660
Db 1131 ATGTATGAAATGATGTGTGGAGGTTTACCTTTCTACAACCCAGGACCATGAGAAACTTTT 1190
QY 661 GAATTAATTAATTAATGGAAGACATTAATAATTTCTCGAACACATCTCTTCAGATGCAAAATCA 720
Db 1191 GAATTAATTAATTAATGGAAGACATTAATAATTTCTCGAACACATCTCTTCAGATGCAAAATCA 1250
QY 721 TTGCTTTCAGGCTCTTCGATAAAGATCCAAATAAAACGCTTTGGTGGAGGACCATGAT 780
Db 1251 TTGCTTTCAGGCTCTTCGATAAAGATCCAAATAAAACGCTTTGGTGGAGGACCATGAT 1310
QY 781 GCAAAAGAAATTAATGAGACACAGATTTTCTCTCGAGTAAACTGGCAAGATGTATATGAT 840
Db 1311 GCAAAAGAAATTAATGAGACACAGATTTTCTCTCGAGTAAACTGGCAAGATGTATATGAT 1370
QY 841 AAAAGCTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 900
Db 1371 AAAAGCTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 1430
QY 901 GATGAAGAAATTAATGAGTCAAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 953
Db 1431 GATGAAGAAATTAATGAGTCAAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 1483
```

RESULT 4

```
US-10-394-568-1
; Sequence 1, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUO, KUN
; APPLICANT: IVASHCHENKO, YURI
; APPLICANT: CLARK, KENNETH L.
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; FILE REFERENCE: A3399WO
; CURRENT APPLICATION NUMBER: US/10/394, 568
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584, 938
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-10-394-568-1

Query Match 97.1%; Score 949.8; DB 6; Length 1570;
Best Local Similarity 99.8%; Pred. No. 2.3e-245;
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 TCTACACCCATCATAAAGAAAGACATGATGATTTTGACTATTGCTATTGCTGAACTACTAGGT 60
Db 531 TCTACACCCATCATAAAGAAAGACATGATGATTTTGACTATTGCTGAACTACTAGGT 590

Qy 61 AAAGGCACCTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATATCTATGCT 120
Db 591 AAAGGCACCTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATATCTATGCT 650

Qy 121 ATGAAGATTTCTGAAGAAAGAGTCAATATTGCAAGAGATGAAGTGGCACACACTCTAACT 180
Db 651 ATGAAGATTTCTGAAGAAAGAGTCAATATTGCAAGAGATGAAGTGGCACACACTCTAACT 710

Qy 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 240
Db 711 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 770

Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 300
Db 771 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 830

Qy 301 CATTTGTGAGAGCGGGTGTCTCTGAGAGCGCACACATGTTTCTATGTTGCAAAAT 360
Db 831 CATTTGTGAGAGCGGGTGTCTCTGAGAGCGCACACATGTTTCTATGTTGCAAAAT 890

Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTTGTACCGTGTATCTCAAGTTGGAG 420
Db 891 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTTGTACCGTGTATCTCAAGTTGGAG 950

Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGCAATGCAAGAA 480
Db 951 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGCAATGCAAGAA 1010

Qy 481 GGGATCAAGATGCGACCAACCATGAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 1011 GGGATCAAGATGCGACCAACCATGAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 1070

Qy 541 GAGTGTAGAAATATGATTAAGAGATCAAAATTTTCTCGAACACTCTCTCAGATGCAAAATCA 720
Db 1191 GAGTGTAGAAATATGATTAAGAGATCAAAATTTTCTCGAACACTCTCTCAGATGCAAAATCA 1250

Qy 721 TTGCTTTTCAGGGCTCTTGATTAAGAGATCAAAATTTTCTCGAACACTCTCTCAGATGCAAAATCA 780
Db 1251 TTGCTTTTCAGGGCTCTTGATTAAGAGATCAAAATTTTCTCGAACACTCTCTCAGATGCAAAATCA 1310

Qy 781 GCAAAAGAAATTTAGACACAGTTTCTTCTCGAGTAAACTCGCAAGATGTATATGAT 840
Db 1311 GCAAAAGAAATTTAGACACAGTTTCTTCTCGAGTAAACTCGCAAGATGTATATGAT 1370

Qy 841 AAAAAGCTTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT 900
Db 1371 AAAAAGCTTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT 1430

Qy 901 GATGAAGAAATTTACAGCTCAGACTATTATCAATATACACCACTGAAATATGA 953
Db 1431 GATGAAGAAATTTACAGCTCAGACTATTATCAATATACACCACTGAAATATGA 1483
```

RESULT 5

US-11-063-691-1
; Sequence 1, Application US/11063691
; Publication No. US20050142603A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Matco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri

; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/11/063.691
; PRIOR FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: US/09/526.043
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/125,108
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-11-063-691-1

Query Match 97.1%; Score 949.8; DB 10; Length 1570;
Best Local Similarity 99.8%; Pred. No. 2.3e-245;
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 TCTACACCCATCATAAAGAAAGACATGATGATTTTGACTATTGCTGAACTACTAGGT 60
Db 531 TCTACACCCATCATAAAGAAAGACATGATGATTTTGACTATTGCTGAACTACTAGGT 590

Qy 61 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATATCTATGCT 120
Db 591 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATATCTATGCT 650

Qy 121 ATGAAGATTTCTGAAGAAAGAGTCAATATTGCAAGAGATGAAGTGGCACACACTCTAACT 180
Db 651 ATGAAGATTTCTGAAGAAAGAGTCAATATTGCAAGAGATGAAGTGGCACACACTCTAACT 710

Qy 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 240
Db 711 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 770

Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 300
Db 771 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 830

Qy 301 CATTTGTGAGAGCGGGTGTCTCTGAGAGCGCACACAGTTTTCTATGTTGCAAAAT 360
Db 831 CATTTGTGAGAGCGGGTGTCTCTGAGAGCGCACACAGTTTTCTATGTTGCAAAAT 890

Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTTGTGTACCGTGTATCTCAAGTTGGAG 420
Db 891 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTTGTGTACCGTGTATCTCAAGTTGGAG 950

Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGCAATGCAAGAA 480
Db 951 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGCAATGCAAGAA 1010

Qy 481 GGGATCAAGATGCGACCAACCATGAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 1011 GGGATCAAGATGCGACCAACCATGAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 1070

Qy 541 GAGTGTAGAAATATGATTAAGAGATCAAAATTTTCTCGAACACTCTCTCAGATGCAAAATGA 600
Db 1071 GAGTGTAGAAATATGATTAAGAGATCAAAATTTTCTCGAACACTCTCTCAGATGCAAAATGA 1130
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QY 601 ATGTATGAATGATGTGGGAGGTACCTTTCTCAACAGGACCATGAGAACTTTT 660
Db 1131 ATGTATGAATGATGTGGGAGGTACCTTTCTCAACAGGACCATGAGAACTTTT 1190
QY 661 GAATTAATTAATGAAGACATTAATTTCTCTGCAACACTCTCTTCAAGATGCAAAATCA 720
Db 1191 GAATTAATTAATGAAGACATTAATTTCTCTGCAACACTCTCTTCAAGATGCAAAATCA 1250
QY 721 TTGCTTTTCAAGGCTCTTATGAAGATCAAATAAAGCGCTTGGTGGAGGACCATGAT 780
Db 1251 TTGCTTTTCAAGGCTCTTATGAAGATCAAATAAAGCGCTTGGTGGAGGACCATGAT 1310
QY 781 GCAAGAAATTAATGAGACACAGTTTCTCTCTGAGTAACTGCAAGATGTATATGAT 840
Db 1311 GCAAGAAATTAATGAGACACAGTTTCTCTCTGAGTAACTGCAAGATGTATATGAT 1370
QY 841 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 900
Db 1371 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 1430
QY 901 GATGAAGAAATTAACAGCTCAGACTATTACAATAACCAACCTGAAAAATATGA 953
Db 1431 GATGAAGAAATTAACAGCTCAGACTATTACAATAACCAACCTGAAAAATATGA 1483

RESULT 6
US-10-887-553A-692
; Sequence 692, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 1703
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-692

Query Match 97.1%; Score 949.8; DB 9; Length 1703;
Best Local Similarity 99.8%; Pred. No. 2.4e-245;
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTACAACCCATCATATAAAGAAAGCAATGAATGATTTTGAATCTATTGAAACTACTAGGT 60
Db 487 TCTACAACCCATCATATAAAGAAAGCAATGAATGATTTTGAATCTATTGAAACTACTAGGT 546
QY 61 AAAGGCACTTTTGGAAAGTTATTTTGGTTGAGAGAAAGGCAAGTGGAAATATCTATGCT 120
Db 547 AAAGGCACTTTTGGAAAGTTATTTTGGTTGAGAGAAAGGCAAGTGGAAATATCTATGCT 606
QY 121 ATGAAGATCTGAAAGAAAGTCAATTTATGCAAGGATGAAGTGGACACACTCTAACT 180
Db 607 ATGAAGATCTGAAAGAAAGTCAATTTATGCAAGGATGAAGTGGACACACTCTAACT 666
QY 181 GAAACGAGATTAATAAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATTTCCCTTC 240
Db 667 GAAACGAGATTAATAAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATTTCCCTTC 726
QY 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTC 300
Db 727 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTC 786
QY 301 CATTTGTCGAGAGAGCGGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAT 360

Db 787 CATTTGTCGAGAGAGCGGGTGTCTCTGAGAGCCGCACACGTTTCTATGGTGCAGAAAT 846
QY 361 GTCTCTGCTTGGACTATCTACATTTCCGAAAGATTTGTGTACCGTGATCTCAAGTTGGAG 420
Db 847 GTCTCTGCTTGGACTATCTACATTTCCGAAAGATTTGTGTACCGTGATCTCAAGTTGGAG 906
QY 421 AATCTAATGCTGGACAAAGATGGCCACATATAAATAATCAGATTTTGGACTTTTGCAGAA 480
Db 907 AATCTAATGCTGGACAAAGATGGCCACATATAAATAATCAGATTTTGGACTTTTGCAGAA 966
QY 481 GGGATCACAGATGAGCCACCATGAAGACATTTCTGTGSCACTCCAGAAATATCTGCACCA 540
Db 967 GGGATCACAGATGAGCCACCATGAAGACATTTCTGTGSCACTCCAGAAATATCTGCACCA 1026
QY 541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGTTGGGGCTTAGGGGTGTGC 600
Db 1027 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGTTGGGGCTTAGGGGTGTGC 1086
QY 601 ATGTATGAATGATGTGGGAGGTACCTTTCTACAACAGGACCATGAGAACTTTT 660
Db 1087 ATGTATGAATGATGTGGGAGGTACCTTTCTACAACAGGACCATGAGAACTTTT 1146
QY 661 GAATTAATTAATGAAGACATTAATTTCTCTGAAACACTCTCTTCAAGTGCAGAAATCA 720
Db 1147 GAATTAATTAATGAAGACATTAATTTCTCTGAAACACTCTCTTCAAGTGCAGAAATCA 1206
QY 721 TTGCTTTTCAAGGCTCTTGTATAAAGGATCAAATAAAGCGCTTGGTGGAGGACCATGAT 780
Db 1207 TTGCTTTTCAAGGCTCTTGTATAAAGGATCAAATAAAGCGCTTGGTGGAGGACCATGAT 1266
QY 781 GCAAAAGAAATTAATGAGACACAGTTTCTCTCTGAGTAAACTGCGCAAGATGTATATGAT 840
Db 1267 GCAAAAGAAATTAATGAGACACAGTTTCTCTCTGAGTAAACTGCGCAAGATGTATATGAT 1326
QY 841 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 900
Db 1327 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 1386
QY 901 GATGAAGAAATTAACAGCTCAGACTATTACAATAACCAACCTGAAAAATATGA 953
Db 1387 GATGAAGAAATTAACAGCTCAGACTATTACAATAACCAACCTGAAAAATATGA 1439

RESULT 7
US-09-771-161A-66
; Sequence 66, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 2410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-66

Query Match 70.4%; Score 689; DB 3; Length 2410;
Best Local Similarity 100.0%; Pred. No. 7.3e-175;
Matches 689; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AGCTGTTTTTCCATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATG 349

Db 312 AGCTGTTTTCATTTCTCGAGAGCGGGTCTCTGAGGACCGCACACGTTTCTATG 371
Qy 350 GTGCAGAAATGTCCTCGCCCTTGACATCTACATTCGGAAAGATTGTGTACCGTGATC 409
Db 372 GTGCAGAAATGTCCTCGCCCTTGACATCTACATTCGGAAAGATTGTGTACCGTGATC 431
Qy 410 TCAAGTTGGAGAACTTAATGCTGGCAAAAGATGGCCACATAAAATTTACAGATTTTGGAC 469
Db 432 TCAAGTTGGAGAACTTAATGCTGGCAAAAGATGGCCACATAAAATTTACAGATTTTGGAC 491
Qy 470 TTTCCAAAGAGGATCACAGATCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAT 529
Db 492 TTTGCCAAAGAGGATCACAGATCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAT 551
Qy 530 ATCTGGCACCAGAGGTGTAGAAGATAATGATGCGCGAGCAGTAGACTGTGGGGGCC 589
Db 552 ATCTGGCACCAGAGGTGTAGAAGATAATGATGCGCGAGCAGTAGACTGTGGGGGCC 611
Qy 590 TAGGGGTTGTCATGATGAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATG 649
Db 612 TAGGGGTTGTCATGATGAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATG 671
Qy 650 AGAACTTTTGAATTAATTAATGAAGACATTAATTTCTCGAACTCTCTTCAG 709
Db 672 AGAACTTTTGAATTAATTAATGAAGACATTAATTTCTCGAACTCTCTTCAG 731
Qy 710 ATGCATAATCATTCCTTCAGGCTCTTGATAAGGATCCAAATAACGCTTGGTGAG 769
Db 732 ATGCATAATCATTCCTTCAGGCTCTTGATAAGGATCCAAATAACGCTTGGTGAG 791
Qy 770 GACCAGATGATGCAAAAGAAATTAAGACACACAGTTTCTCTCGAGTAAACTGGCAAG 829
Db 792 GACCAGATGATGCAAAAGAAATTAAGACACACAGTTTCTCTCGAGTAAACTGGCAAG 851
Qy 830 ATGATATGATAAAAGCTTGACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 889
Db 852 ATGATATGATAAAAGCTTGACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 911
Qy 890 CTAGATATTTTGATGAAGATTTACAGCTCAGACTATTACAAATAACACCTCGAAAAAT 949
Db 912 CTAGATATTTTGATGAAGATTTACAGCTCAGACTATTACAAATAACACCTCGAAAAAT 971
Qy 950 ATGATGAGGATGGTATGAGCTGCATGGAC 978
Db 972 ATGATGAGGATGGTATGAGCTGCATGGAC 1000

RESULT 8

US-10-322-281-412
; Sequence 412, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-322-281-412
Query Match 53.9%; Score 527; DB 7; Length 1722;
Best Local Similarity 72.7%; Pred. No. 3.3e-131;
Matches 680; Conservative 0; Mismatches 255; Indels 0; Gaps 0;
Qy 19 AGAAGACAATGAATGATTTTGACTATTGTGAACATCTAGGTAAGGCACCTTTGGGAAA 78

RESULT 9

US-10-324-985A-2
; Sequence 2, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; CURRENT FILING DATE: 2002-12-19

Db 651 AAAGTGACCATGAATGACTTTCGATTATCTCAAACTCTCTCGGCAAGGCGACCTTCGGCAAG 710
Qy 79 GTTATTTTGTTCGAGAGGCAAGTGGAAAAATACCTATCTATGAAAGATTCTGAAGAAA 138
Db 711 GTCAATCTGGTTCGAGAGAGGCGCACTGGCCGCTATTATGCCATGAAGATCTTCGCGAAG 770
Qy 139 GAAGTCATTTATTCGAAAGGATGAAGTGGCACACACTCTAACTGAAGACAGAGATTAAAG 198
Db 771 GAGGTCACTATTGCAAAAGGATGAAGTGGCCACACACAGTCAACAGAGACCGGGTCTCGAG 830
Qy 199 AACACTAGACATCCCTTTTAAACATCTTGAATATTCCTTCCAGACAAAAGACCGTTTG 258
Db 831 AATACGAGGACCCCTTCTTTACAGCCCTCAAGTATGCTTCCAGATCCCATGACCGCCTA 890
Qy 259 TGTCTTGTGATGAAATATGTTAATGGGGCGAGCTGTCTTTTCCATTTGTTCGAGAGACGG 318
Db 891 TGTCTTGTGATGAGTATGCCACGGGGTGAGCTGTCTTTCCACCTCTCTCGGAGGGA 950
Qy 319 GTCTTCTTCGAGACCGCACACGTTTCTATGTTGTCAGAAAATTTGTCTCTGCTTGGACTAT 378
Db 951 GTCTTTCAGGAGGATCGGGCGCTTTTATGGAGCAGAGATTGTGTCACTCTCGAGTAT 1010
Qy 379 CTACATTCGGAAGAGATTGTGTACCGTGATCTCAAGTTGAGAAATCTAATGCTGGACAAA 438
Db 1011 TTGCATCTCGAGAGATGTGGTGTACCGTGACATCAAGCTGGAAAACCTTATGTTGGACAAA 1070
Qy 439 GATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAAAGGATCAACAGATGACGCC 498
Db 1071 GATGGCCACATCAAGATCACTGACTTTGGCTTTGCAAGAGGCGCATCAGTGATGGAGCC 1130
Qy 499 ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACACAGAGTGTGTAGAGATAAT 558
Db 1131 ACCATGAAGACATTTCTGTGGTACCCCGAGTACTTGGCGCTGAGGTGCTAGAGACAAAT 1190
Qy 559 GACTATGCGCGAGCAGTAGACTGTGGGGCTTAGGGTTCATGATGAATGATGATCTGT 618
Db 1191 GACTATGCGCGAGCAGTAGACTGTGGGGCTTAGGGTTCATGATGAATGATGATGATGTGT 1250
Qy 619 GGGAGGTTACTTTCTACAAACCCAGGACCATGAGAAAACCTTTTGAATTAATTAATGAAA 678
Db 1251 GGGCGCTGCCATTTCTACAAACCCAGGACCCAGGCGCTCTTTGAGCTCAITTTATGGAG 1310
Qy 679 GACATTAATTTCTTCGAAACACTCTCTTCAGATGCAAAAATCAITTTTCAGGGCTCTTG 738
Db 1311 GAGATCGCTTCCCGCGCACACTCGGGCCAGAGGCCAAAGTCCCTGCTGGCTGGAGTCTG 1370
Qy 739 ATAAAGATCCAAATAAACCGCTTGGTGGAGGACCATGATGTCAAAAGAAATTAATGAGA 798
Db 1371 AAGAAGGACCCAAAGCAGAGGCTCGGGGAGGTCCTCAGTGTGCAAGGAGGTCAATGGAG 1430
Qy 799 CACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAAAGCTTGTACCTCCT 858
Db 1431 CATAGATTTCTCTCAGCATCACTGGCAGGACGTGGTACAGAAAAGCTCTGCCACCC 1490
Qy 859 TTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTTGTATGAAGAAATTTACAGCT 918
Db 1491 TTTAAACCTCAGGTCACTTCAGAAAGTGGACACAAAGGTACTTTGATGACGAGTTCACGCC 1550
Qy 919 CAGACTATTACATAACACCCCTGAAAAATATGA 953
Db 1551 CAGTCCATCAAAATCACACCCCCCAGACCGCATATGA 1585


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; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1741
; TYPE: DNA
; ORGANISM: mouse
US-10-324-985A-2

Query Match      53.9%; Score 527; DB 6; Length 1741;
Best Local Similarity 72.7%; Pred. No. 3.3e-131;
Matches 680; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 19 AGAAGACAATGAATGATTTGACTATTTGAACTACTAGTAAAGGACACTTTGGGAAA 78
Db 652 AAAGTGACCATGAATGACTTCGATTATCTCAAACTCTCGGCAAGGACCTTCGGCAAG 711
QY 79 GTTATTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATCTGAAGAAA 138
Db 712 GTCATTCTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATCTGAAGAAA 771
QY 139 GAAAGTCATTATTTGCAAAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTAAGA 198
Db 772 GAGGTTCATCATTTGCAAAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTAAGA 831
QY 199 AACACTAGACATCCCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCT 258
Db 832 AATACGAGGACCCCTTCTTACAGCCCTCAAGTATGCTTCCAGACCCATGACCGCCTA 891
QY 259 TGTCTTCTGAGGATGATATGTTAAAGTGGGGGCGAGCTTTTCCATTTCTCGAGAGAGGG 318
Db 892 TGTCTTCTGAGGATGATATGTTAAAGTGGGGGCGAGCTTTTCCATTTCTCGAGAGAGGG 951
QY 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATTTCTCTGCTTGGACTAT 378
Db 952 GTCATTCTGAGGATGATATGTTAAAGTGGGGGCGAGCTTTTCCATTTCTCGAGAGAGGG 1011
QY 379 CTACATTCGGGAAAGATTTGTGTACCGGTATCTCAAGTTGGAGAAATCTAATGCTGGACAAA 438
Db 1012 TTGCACTCGAGAGATGTTGTGTACCGGTATCTCAAGTTGGAGAAATCTAATGCTGGACAAA 1071
QY 439 GATGGCCACATPAAAAATTTACAGATTTTGGATCTTTTGGCAAAAGGAGATCAGATCGAGCC 498
Db 1072 GATGGCCACATPAAAAATTTACAGATTTTGGATCTTTTGGCAAAAGGAGATCAGATCGAGCC 1131
QY 499 ACCATGAAGACATTTCTGAGGACCTCCAGAAATATCTGGCACACAGAGGTGTGAAGATAT 558
Db 1132 ACCATGAAGACATTTCTGAGGACCTCCAGAAATATCTGGCACACAGAGGTGTGAAGATAT 1191
QY 559 GACTATGCGCGAGCAGTATGAGTGTGGGGGCGCTAGGGGTTGTGCTATGTAATGATGTGT 618
Db 1192 GACTATGCGCGAGCAGTATGAGTGTGGGGGCGCTAGGGGTTGTGCTATGTAATGATGTGT 1251
QY 619 GGGAGTTTACCTTTCTACACAGACCCATGAGAACTTTTGAATTAATTAATGAAA 678
Db 1252 GGGAGTTTACCTTTCTACACAGACCCATGAGAACTTTTGAATTAATTAATGAAA 1311
QY 679 GACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTCTTTCAGGGGCTTTG 738
Db 1312 GAGATTCGGCTTCCGGGACACTCGGGGCGAGGCTCCAGTGTATGCGAAGGAGTCAATGAG 1371
QY 739 ATAAAGGATCCAAATAAACCGCTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGA 798
Db 1372 AAGAAGGATCCAAATAAACCGCTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGA 1431
QY 799 CACAGTTTCTTCTGAGGATTAACCTGGCAGAGTGTATGATGAAAAAGGTTGACTCTCT 858
Db 1432 CATAGATTTCTTCTGAGGATTAACCTGGCAGAGTGTATGATGAAAAAGGTTGACTCTCT 1491
QY 859 TTTAAACCTCAAGTAACTCTCAGACAGATATCTAGATATTTTGTGAAGAAATTTACAGCT 918
Db 1492 TTTAAACCTCAAGTAACTCTCAGACAGATATCTAGATATTTTGTGAAGAAATTTACAGCT 1551
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QY 919 CAGACTATTACAATAACACACACCTGAAAAATATGA 953
Db 1552 CAGTCCATCACAATCACACCCCGACCGATATGA 1586

RESULT 10
US-10-735-461-21
; Sequence 21, Application US/10735461
; Publication No. US20050014264A1
; GENERAL INFORMATION:
; APPLICANT: CZECH, Michael P.
; APPLICANT: ZHOU, Qionglin
; APPLICANT: JIANG, Zhen
; TITLE OF INVENTION: METHOD OF INTRODUCING siRNA INTO
; FILE REFERENCE: UMY-055
; CURRENT APPLICATION NUMBER: US/10/735,461
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: 60/432427
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1741
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-735-461-21
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Query Match      53.9%; Score 527; DB 8; Length 1741;
Best Local Similarity 72.7%; Pred. No. 3.3e-131;
Matches 680; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 19 AGAAGACAATGAATGATTTTGAATTTGAACTACTAGTAAAGGACACTTTTGGGAAA 78
Db 652 AAAGTGACCATGAATGACTTCGATTATCTCAAACTCTCGGCAAGGACCTTCGGCAAG 711
QY 79 GTTATTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATCTGAAGAAA 138
Db 712 GTCATTCTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATCTGAAGAAA 771
QY 139 GAAAGTCATTATTTGCAAAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTAAGA 198
Db 772 GAGGTTCATCATTTGCAAAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTAAGA 831
QY 199 AACACTAGACATCCCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCT 258
Db 832 AATACGAGGACCCCTTCTTACAGCCCTCAAGTATGCTTCCAGACCCATGACCGCCTA 891
QY 259 TGTCTTCTGAGGATGATATGTTAAAGTGGGGGCGAGCTTTTCCATTTCTCGAGAGAGGG 318
Db 892 TGTCTTCTGAGGATGATATGTTAAAGTGGGGGCGAGCTTTTCCATTTCTCGAGAGAGGG 951
QY 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATTTCTCTGCTTGGACTAT 378
Db 952 GTCATTCTGAGGATGATATGTTAAAGTGGGGGCGAGCTTTTCCATTTCTCGAGAGAGGG 1011
QY 379 CTACATTCGGGAAAGATTTGTGTACCGGTATCTCAAGTTGGAGAAATCTAATGCTGGACAAA 438
Db 1012 TTGCACTCGAGAGATGTTGTGTACCGGTATCTCAAGTTGGAGAAATCTAATGCTGGACAAA 1071
QY 439 GATGGCCACATPAAAAATTTACAGATTTTGGATCTTTTGGCAAAAGGAGATCAGATCGAGCC 498
Db 1072 GATGGCCACATPAAAAATTTACAGATTTTGGATCTTTTGGCAAAAGGAGATCAGATCGAGCC 1131
QY 499 ACCATGAAGACATTTCTGAGGACCTCCAGAAATATCTGGCACACAGAGGTGTGAAGATAT 558
Db 1132 ACCATGAAGACATTTCTGAGGACCTCCAGAAATATCTGGCACACAGAGGTGTGAAGATAT 1191
QY 559 GACTATGCGCGAGCAGTATGAGTGTGGGGGCGCTAGGGGTTGTGCTATGTAATGATGTGT 618
Db 1192 GACTATGCGCGAGCAGTATGAGTGTGGGGGCGCTAGGGGTTGTGCTATGTAATGATGTGT 1251
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Qy 619 GGGAGGTTACCTTTCTCAACACGAGCAGATGAGAAAATTTTGAATTAATTAATCGAA 678
Db 1252 GCGCGCTGCCATTTCTACACGAGGACACGAGCGCTCTTTGAGCTCAATTTATGGAG 1311
Qy 679 GACATTAATTTCTCGAAGCACTCTCTTCAGATCGAAATCATTTGCTTTAGGGCTTTG 738
Db 1312 GAGATCCGCTTCCCGCGCACACTCGGCCAGAGGCCAAGTCCCTGCTGGCTGGACTGCTG 1371
Qy 739 ATAAGGATCCAAATAAAGCGCTTTGGTGGAGGACAGATGATGACAAAGAAATTTATGAGA 798
Db 1372 AAGAAGACCCAAAGCAGAGGCTCGGCGAGGTCCTCAGTGTATGCAAGAGGTCATGGAG 1431
Qy 799 CACAGTTTCTCTCGGAGTAAACTGCGCAAGATGATATATGATATAAAGCTTTGACCTCCT 858
Db 1432 CATAGATTTCTCTCAGCATCAACTGGCAGGACGCTGGGTACAGAAAAGCTCTGCCACCC 1491
Qy 859 TTTAAACCTCAAGTAAACATCTGACACAGATCTAGATATTTTGATGAAGAAATTTACAGCT 918
Db 1492 TTCAACCTCAGGTCACTTCAGAAAGTGGACACAAGGTACTTTGATGACGAGTTCCACGCC 1551
Qy 919 CAGACTATTACAATAACACCACTGAAAAATATGA 953
Db 1552 CAGTCCATCAATCACACCCCGAGCGATATGA 1586

RESULT 11

US-10-895-225A-57
; Sequence 57, Application US/10895225A
; Publication No. US20050048587A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; APPLICANT: Snyder, Jessica
; APPLICANT: Bagley, Andrea
; TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
; TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: TILN-025
; CURRENT APPLICATION NUMBER: US/10/895,225A
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/488,502
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 3010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-895-225A-57

Query Match 53.9%; Score 527; DB 9; Length 3010;
Best Local Similarity 72.7%; Pred. No. 4.4e-131;
Matches 680; Conservative 0; Mismatches 255; Indels 0; Gaps 0;
Qy 19 AGAAGACATGAATGATTTTGACTATTGAACTACTAGTAAAGGCACTTTGGGAAA 78
Db 622 AAAGTGACCATGAATGATCTCGATTATCTCAAACTCTCGGCAAGGCGCACTTCGGCAAG 681
Qy 79 GTTATTTTGGTTCGAGAGGCAAGTGGAAATACTATGCTATGAAGATTCTGAAGAAA 138
Db 682 GTCATTTGGTTCGAGAGAGGCCACTGGCCGCTATTATGCCATGAAATCCTCGGCAAG 741
Qy 139 GAAGTCATTAATGCAAGGATGAAGTGGGCAACACTCTAACTGAAAGCAGATTAAGAAG 198
Db 742 GAGTCCATTAATGCAAGGATGAAGTGGCCACACAGTCACAGAGAGCGCGGTTCTCGAG 801
Qy 199 AACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTCAGACAAAGACCGTTTG 258
Db 802 AATACAGGCAACCCCTTCTTACAGCCCTCAAGTATGCTTCCAGACCCCATGACCGCCTA 861
Qy 259 TGTTTTGTGATGAATATGTTAAATGGGGCGGAGCTGTTTTTCCATTTTGTGAGAGAGCGG 318
Db 862 TGTCTTGTGATGGAGTATGCCACGGGGGTGAGCTGTTTTTCCACCTCTCTCGGAGCGGA 921
Qy 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTTGCTCTGCGCTTGGACTAT 378

Db 922 GTCTTCACGAGGATCGGGCGCGCTTTTATGGAGCAGAGATTGTGTGAGCTCTGGAGTAT 981
Qy 379 CTACATTCGGAAGAGATTGTACCGTGTACTCAAGTTGGAGATCTAAATGCTGGACAAA 438
Db 982 TTGACCTCGAGAGATGTTGGTGTATCCGCTGACATCAAGCTGGAAACCTTATGTTGGACAAA 1041
Qy 439 GATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAGGATCAAGATGACAGCC 498
Db 1042 GATGGCCACATCAAGATCACTGACTTTGGCTTTGCAAGAGGCGATCAGTGATGGAGCC 1101
Qy 499 ACCATGAAGACATTTCTGTGGCACTTCCAGAAATATCTGGCACAGAGGTGTTAGAAAGATAAT 558
Db 1102 ACCATGAAACCTTCTGTGGTACCCCGGAGTACTTGGCGCTGAGGTGCTAGAGGACAAAT 1161
Qy 559 GACTATGGCCGACAGTACAGTGGTGGCGCTAGGGTGTGCTATGATGAATGATGCTGT 618
Db 1162 GACTATGGCGGACAGTGGACTGGTGGGGCTGGGTGTGCTATGATGAGATGATGTGT 1221
Qy 619 GGGAGGTTTACCTTTCTACAAACACGAGCACCATGAGAAAATTTTGAATTAATTAATGAAA 678
Db 1222 GCGCGCTGCCATTTCTACAAACACGAGCACCAGCGGCTCTTTGAGCTCAITCTTATGGAG 1281
Qy 679 GACATTAATTTCTCGAAGCACTCTCTTCAGATGCAAAATCATTTGCTTTAGGGCTCTTG 738
Db 1282 GAGATCCGCTTCCCGCGCACACTCGGCGCCAGAGGCCAAAGTCCCTGCTGGCTGGACTGCTG 1341
Qy 739 ATAAAGGATCCAAATAAAGCGCTTTGTGGAGGACAGATGATGCAAAAGAAATTAATGAGA 798
Db 1342 AAGAAGACCCAAAGCAGAGGCTCGGCGGAGGTCCTAGTATGCGAAGGAGGTCATGGAG 1401
Qy 799 CACAGTTTCTCTCGAGTAAACTGCGAAGATGTATATGATATAAAGCTTTGACCTCCT 858
Db 1402 CATAGATTTCTCTCAGCATCAACTGGCAGGACGTGGTACAGAAAAGCTCTGCGCACCC 1461
Qy 859 TTTAAACCTCAAGTAACTCTGAGACAGATACCTAGATATATTTTGGATGAAGAAATTTACAGCT 918
Db 1462 TTTAAACCTCAGGTCACTTTCAGAAAGTGGACACAAAGGTACTTTGATGACGAGTTCCACGCC 1521
Qy 919 CAGACTATTACAATAACACCCCTGAAAAATATGA 953
Db 1522 CAGTCCATCAATCAACACCCCGAGCGGATATGA 1556

RESULT 12

US-10-324-985A-5
; Sequence 5, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US1/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: mouse
US-10-324-985A-5

Query Match 53.7%; Score 525; DB 6; Length 1140;
Best Local Similarity 73.4%; Pred. No. 9.1e-131;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;
Qy 24 GACAATGAATGATTTTGGACTATTGAACTACTAGGTAAAGGCACTTTTGGGAAAGTTAT 83
Db 135 GACCATGAACGAGTTTGGTACCTGAACTACTGGGCAAGGCGCACCTTTGGGAAAGTAT 194
Qy 84 TTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAGATTTCTGAAGAAAGAAGT 143

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Db 195 TCTGTGAAAGAGAGGCCACAGGCGCTACTATGTCATGAAGATCCTCAAGAGAGGT 254
Qy 144 CATTATGCAAAAGGATGAAGTGGCCACACACTCTAACTGAAGCAGAGTATTAAAGAACAC 203
Db 255 CATCGTCGCCAAGGATGAGTTGCCACACGCTTACTGAGAACCGTGCTCGACGAACCTC 314
Qy 204 TAGACATCCCTTTTAAACATCCTTGAATATTCCTTCAGACAAAAGACCGTTGTGTTT 263
Db 315 TAGGCATCCCTTCTTACGGCCCTCAAGTACTCAATTCACAGACCCACGCGCTCTGCTT 374
Qy 264 TGTGATGGAATATGTTAATGCGGGCGAGCTGTTTTCATTTGTCAGAGAGCGGCTGTT 323
Db 375 TGTCTAGGATGATGCCAAGCGGGCGAGCTCTCTCCACCTGTCTCGAGAGCGGCTGTT 434
Qy 324 CTCTGAGGACCCGACACGTTTCTATGGTGCAGAAATGTTCTGCTTGGACTATCTACA 383
Db 435 CTCGAGGACCGGGCCCGCTTCTATGGTGCAGAGATTTGTCTGCGCTGGACTACTTGCA 494
Qy 384 TTCGGAAGA---TTGTGTACCGTGAATCTCAAGTTGGAGATCTAATGCTGGACAAAGA 440
Db 495 CTCGAGAGAACGTTGGTGTACCGGACCTGAAGCTGGAGAACCTCATGCTGGACAAAGA 554
Qy 441 TGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAGAGGATCACAGATGCGAGCCAC 500
Db 555 CGGGCACATCAAGATAACGAGCTTCGGGCTGTGCAAGAGGGGATCAAGGATGGTGCCAC 614
Qy 501 CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACGAGAGTGTAGAGATAATGA 560
Db 615 TATGAAGACATTTCTGGGAACCGGAGTACCTGGCCCTGAGGTGCTGGAGGACACGA 674
Qy 561 CTATGCGCAGAGTAGTACTGTGGGCTTACGGGCTTACGGGCTTATGATGAAATGATGTGG 620
Db 675 CTACGGCGCTGCAGTGGACTGTGTGGGGCTGGGCGTGTGATGATGATGATGTGTGG 734
Qy 621 GAGGTTACTCTTCTACACACGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
Db 735 CCGCTTGCCTTCTACACACGACCATGAGAACTGTTCGAGCTGATCCTCATGGAGGA 794
Qy 681 CATTAAATTTCTCGAACAACCTCTTTCAGATGCAAAATCATTTGCTTTCAGGCGCTCTTGAT 740
Db 795 GATCGCTTCCCGCGCACACTCGGCCCTGAGGCCAAGTCCCTGCTCTCGGCGCTCTCA 854
Qy 741 AAAGATCAAAATAAACGCTTGTGGAGGACCAAGATGCAAAAGAAATTTATGAGACA 800
Db 855 GAAAGACCTTACACAGAGGCTCGGTGGGGCTCTGAGGATGCAAGAGGATCATGCAGCA 914
Qy 801 CAGTTTCTTCTCTGGAGTAAATGCGCAAGATGATATGATATAAAGCTTGTAACCTCTTT 860
Db 915 CCGGTTCTTTTGCACAACATCGTGTGGCAGGATGTGATGAGAAAGAGCTGAGCCACCTTT 974
Qy 861 TAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTTGAATGAAGAAATTTACAGCTCA 920
Db 975 CAAGCCCGAGGTCACTCTGAGACTGACACACAGGTATTTTCGATGAGGAGTTCCAGCTCA 1034
Qy 921 GACTATTACAATAACACCACTGAAATAATGA 953
Db 1035 GATGATCACCATCACGCGCGCTGATCAAGATGA 1067
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RESULT 13

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US-11-166-990-66
; Sequence 66, Application US/11166990
; Publication No. US20050239125A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Timothy A.
; TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING
; FILE REFERENCE: 023131.41500
; CURRENT APPLICATION NUMBER: US-11/166,990
; PRIOR FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/230,371
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 09/945,952
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; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Mus sp.
US-11-166-990-66
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Query Match 53.7%; Score 525; DB 10; Length 1443;
Best Local Similarity 73.4%; Pred. No. 1e-130;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;
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Qy 24 GACATGAATGATTTTGAATTTGAAACTACTAGGTAAAGCCTTTTGGAAAGTTAT 83
Db 435 GACCATGAACGAGTTTGAATGTTGAAACTACTAGGCAAGGCGCACCTTTTGGAAAGTTAT 494
Qy 84 TTTGTTTCAGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAGAAAGAGT 143
Db 495 TCTGTGAAAGAGAGAGGCCACAGCGCGTACTATGCCATGAAGATCCTCAAGAGAGAGT 554
Qy 144 CATTATTGCAAAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGAACAC 203
Db 555 CATCGTCGCCAAGGATGAGTTGCCACACACGCTTACTGAGAACCGTGTCTGCAGAACCTC 614
Qy 204 TAGACATCCCTTTTAAACATCCTTTGAAATATTTCTTCAGACAAAGAACCGTTTGTGTTT 263
Db 615 TAGGCATCCCTTCTTACGGCCCTCAAGTACTCAATTCAGAGACCCACGACCGCTCTGCTT 674
Qy 264 TGTGATGGAATATGTTAATGAGGCGAGCTGTTTTCATTTGTCAGAGAGCGGCTGTT 323
Db 675 TGTCAATGAGTATGCCAACGGGGGCGAGCTCTTCTTCACCTGTCTCGAGAGCGGCTGTT 734
Qy 324 CTCTGAGGACCGCACACACGTTTCTATGGTGCAGAAATTTGCTCTGCTTGGACTATCTACA 383
Db 735 CTCGAGGACCGGGCCCGCTTCTATGGTGCAGAGATTTGCTCTGCTTGGACTACTTGA 794
Qy 384 TTCGGAAGA---TTGTGTACCGTGAATCTCAAGTTGGAGAAATCTAATGCTGGACAAAGA 440
Db 795 CTCGAGAGAACGCTGTGTACTCGGACCTCAAGCTGGAGAACCTCATGCTGGACAAAGA 854
Qy 441 TGGCCACATAAAATTTAGAGTTTTGGACTTTGCAAGAGAGGATCACAGATGCGAGCCAC 500
Db 855 CGGGCACATCAAGATAACGAGCTTCGGGCTGTGCAAGAGGAGGATCAAGGATGGTGCCAC 914
Qy 501 CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAAAGATAATGA 560
Db 915 TATGAAGACATTTCTGGGAACCGCGGAGTACTTGGCCCTGAGGTGCTGGAGGACACGA 974
Qy 561 CTATGCGCAGCAGTAGACTCGTGGGCGCTTAGGGGTTGTCATGATGAAGAAATGATGTGG 620
Db 975 CTACGGCGCTGCAGTGGACTGTGTGGGGCTGGGCGTGTGATGATGATGATGATGTGG 1034
Qy 621 GAGGTTACTCTTCTACACACGAGGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
Db 1035 CCGCTTGCCTTCTACAAACGAGGACCCAGAGCTGTTTCGAGCTGATCCTCATGGAGGA 1094
Qy 681 CATTAAATTTCTCGAACACACTCTTTCAGATGCAAAATCATTTGCTTTCAGGCGCTCTTGAT 740
Db 1095 GATCGCTTCCCGGCACACTCGGCCCTGAGGCCAAGTCCCTGCTCTCGGGCTGCTCA 1154
Qy 741 AAAGATCCAAATAAACCGCTTGTGGAGGACCAAGATCATGCAAAAGAAATTTATGAGACA 800
Db 1155 GAAGGACCTTACACAGAGGCTCGGTGGGGCTCTGAGGATGCAAGGAGATCATGCAGCA 1214
Qy 801 CAGTTTCTTCTCTGGAGTAAACTGGCAAGATGATATGATATAAAGCTTGTACCTCTTT 860
Db 1215 CCGGTTCTTTTCCCAACATCGTGTGGCAGGATGTGATGAGAAAGAGCTGAGCGCCACTTT 1274
Qy 861 TAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTTGAATGAAGAAATTTACAGCTCA 920
Db 1275 CAAGCCCGAGGTCACTCTGAGACTGACACCGAGGTATTTTCGATGAGGAGTTCCAGCTCA 1334
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Qy 921 GACTATTACATTAACACACCACCTGAAATAATGA 953
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Db 1335 GATGATCACCATCATCGCGCCTGATCAAGATGA 1367

RESULT 14
US-10-324-985A-1
; Sequence 1, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US1/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: mouse
US-10-324-985A-1

Query Match 53.7%; Score 525; DB 6; Length 2626;
Best Local Similarity 73.4%; Pred. No. 1.4e-130;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

Qy 24 GACAATGAATGATTTGACTATTTGAACTACTAGTAAAGGCACTTTTGGGAAAGTTAT 83
|||
Db 718 GACCATGAACGAGTTGAGTACCTGAACTACTGGCAAGGGCACCTTTGGGAAAGTTAT 777

Qy 84 TTTGGTTCCGAGAGCCAGTGAATAACTATGCTATGAGATTCTGAAGAAGT 143
|||
Db 778 TCTGGTGAAGAAGAGGCCACAGCCGCTACTATGCCATGAAGATCCTCAAGAAGAGGTT 837

Qy 144 CATTATTGCAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGAACAC 203
|||
Db 838 CATCGTCGCCAAGATGAGGTTGCCACACGCTTACTGAGAACCGTGTCTGCGAAGACTC 897

Qy 204 TAGACATCCCTTTTAAACATCTTTGAAATATTCCTCCAGACAAAGACCGTTTGTGTTT 263
|||
Db 958 TGTATGGATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGAGCGGGTGT 323

Qy 958 TGTATGGATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGAGCGGGTGT 1017
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Qy 324 CTCTGAGGACCGCACACGTTTCTATGTCGAGAAATGTCCTGCGCTTGACTATCTACA 383
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Db 1018 CTCCGAGGACCGGGCGGCTTCTATGTCGAGATGTTGTCGCGCTTGACTACTTGA 1077

Qy 384 TTCCGGAAGA---TTGTTACCGTGTATCAAGTTGGAGATCTAATGCTGGACAAAGA 440
|||
Db 1078 CTCCGGAAGAAGCTGGTGTACCGGACCTGAAGCTGGAGAACCTCATGCTGGACAAGGA 1137

Qy 441 TGGCCACATATAAATACAGATTTTGACITTTGCAATGCAAGAGGATCACATGACGCCAC 500
|||
Db 1138 CGGCAACATCAAGATAACGAGCTTCGGGCTGTGAAGGAGGGGATCAAGGATGTTGCCAC 1197

Qy 501 CATGAAGACATCTGTGTCACCTCCAGAAATATCTGGCACAGAGGTGTTAGAAGATAATGA 560
|||
Db 1198 TATGAAGACATCTGTGTCACCGGAGTACTTGGCCCTGAGGTGTCGAGGACACAGA 1257

Qy 561 CTATGGCGGACGATGAGTGGTGGGCGCTTGGGCTTGTATGATGAAATGATGTGTGG 620
|||
Db 1258 CTACGGCGGTGACGTGGTGGTGGGCTGGGCGTGGTGTATGATGATGATGTGTGG 1317

Qy 621 GAGTTTACCTTTCTACACCGAGGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
|||
Db 1318 CCGCTGCCCCCTTCTACACCGAGGACCGAAGCTGTTCGAGCTGATCTCTCATGGAGGA 1377
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Qy 681 CATTAAATTTCTTCGAACACTCTTTTCAGATGCAAAATCATTTCTTCAGGGCTCTTGTAT 740
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Db 1378 GATCCGCTTCCCGCGCACACTCGGCCCTGAGGCCAAGTCCCTCTCTCCGGGCTGCTCAA 1437

Qy 741 AAAGGATCCAAATAAAGCCCTTGGTGGAGGACCAGATGATGCAAAAGAAATATGAGACA 800
|||
Db 1438 GAAGGACCCCTACACAGAGGCTCGGTGGGGCTCTGAGGATGCCAAGGAGATCATGACACA 1497

Qy 801 CAGTTTCTCTCTGGAGTAACTGGCAAGATGATATGATAAAAGCTTGTACCTCCTTT 860
|||
Db 1498 CCGTTTCTTGGCAACATCTGTGGCAGGATGTTATGAGAAGAGCTGAGCCACCTTT 1557

Qy 861 TAAACCTCAAGTAAACATCTGAGACAGATAGATATTTTGTGAAGAAATTTACAGCTCA 920
|||
Db 1558 CAAGCCCGAGGTCACTCTGAGACTGACACCCAGGTATTTTCGATGAGGAGTTACAGCTCA 1617

Qy 921 GACTATTACAAATAACACCACCTGAAATAATGA 953
|||
Db 1618 GATGATCACCATCATCGCCGCTGATCAAGATGA 1650

RESULT 15
US-10-713-678-5
; Sequence 5, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10/713,678
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-713-678-5

Query Match 53.7%; Score 525; DB 7; Length 2626;
Best Local Similarity 73.4%; Pred. No. 1.4e-130;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

Qy 24 GACAATGAATGATTTTGAACATTTTGAACCTACTAGGTAAAGGCACTTTTGGGAAAGTTAT 83
|||
Db 718 GACCATGAACGAGTTTGAATGATCTGAACTACTGGGCAAGGGCACCTTTGGGAAAGTTAT 777

Qy 84 TTTGGTTCCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAGAAGTAT 143
|||
Db 778 TCTGGTGAAGAAGAGAGGCCACAGCCGCTACTATGCCATGAAGATCCTCAAGAAGAGGTT 837

Qy 144 CATTATTGCAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGAACAC 203
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Db 838 CATCGTCGCCAAGATGAGGTTGCCACACGCTTACTGAGAACCGTGTCTGCGAAGACTC 897

Qy 204 TAGACATCCCTTTTAAACATCTTTGAAATATTCCTCCAGACAAAGACCGTTTGTGTTT 263
|||
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Qy 264 TGTGATGATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGAGCGGGTGT 323
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Db 958 TGTGATGATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGAGCGGGTGT 1017

Qy 324 CTCTGAGGACCGCACACGTTTCTATGTCGAGAAATGTCCTGCGCTTGACTATCTACA 383
|||
Db 1018 CTCCGAGGACCGGGCGGCTTCTATGTCGAGATGTTGTCGCGCTTGACTACTTGA 1077

Qy 384 TTCCGGAAGA---TTGTTACCGTGTATCAAGTTGGAGATCTAATGCTGGACAAAGA 440
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Db 1078 CTCCGGAAGAAGCTGGTGTACCGGACCTGAAGCTGGAGAACCTCATGCTGGACAAGGA 1137

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Db 1138 CGGCAACATCAAGATAACGAGCTTCGGGCTGTGAAGGAGGGGATCAAGGATGTTGCCAC 1197

Qy 501 CATGAAGACATCTGTGTCACCTCCAGAAATATCTGGCACAGAGGTGTTAGAAGATAATGA 560
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Db 1198 TATGAAGACATCTGTGTCACCGGAGTACTTGGCCCTGAGGTGTCGAGGACACAGA 1257

Qy 561 CTATGGCGGACGATGAGTGGTGGGCGCTTGGGCTTGTATGATGAAATGATGTGTGG 620
|||
Db 1258 CTACGGCGGTGACGTGGTGGTGGGCTGGGCGTGGTGTATGATGATGATGTGTGG 1317

Qy 621 GAGTTTACCTTTCTACACCGAGGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
|||
Db 1318 CCGCTGCCCCCTTCTACACCGAGGACCGAAGCTGTTCGAGCTGATCTCTCATGGAGGA 1377
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Db 1078 CTCGAGAGACGTGGTGTACCGGGACCTGAAGCTGGAGAACCTCATGCTGGACAAGGA 1137
QY 441 TGGCCACATAAAAAATTACAGATTTTGGACTTTGCAAAAGAGGATCACAGATGCAGCCAC 500
Db 1138 CGGGCACATCAAGATAACCGACTTCGGGCTGTGCAAGGAGGGGATCAAGGATGTGCGCAC 1197
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Db 1198 TATGAAGACATTTCTGCGGAACCCCGAGGTACCTGGCCCCGTGAGGTGCTGGAGGACAAGGA 1257
QY 561 CTATGGCCGAGCAGTAGACTGTGGGGCTTAGGGGTTGTATGTATGAAATGATGTGTGG 620
Db 1258 CTACGGCCGTGAGTGAATGTGGGGCTGGCGTGGTCAATGATGAGATGATGTGTGG 1317
QY 621 GAGGTACCTTTCTACAACACAGGACCATGAGAAACTTTTGAATTAATTAATGGAAGA 680
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QY 681 CATTAAATTTCTCGAACAATCTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTCTTGAT 740
Db 1378 GATCGGCTTCCCGCGACACTCGGGCCCTGAGGCCAAGTCCCTGCTCTCGGGCTGCTCAA 1437
QY 741 AAAGGATCCAAATAAAGCGCTTTGGTGGAGGACAGATGATGCAAAAGAAATTAAGAGCA 800
Db 1438 GAAGGACCTTACACAGAGGCTCGGTGGGGCTCTGAGGATGCCAAGGAGATCATGAGCA 1497
QY 801 CAGTTTCTTTCTGAGGTAAACTGGCAAGATGTATATGATAAAAGCTTTGTACCTCCTTT 860
Db 1498 CCGGTTCTTTGCCAACATCGTGTGCGAGGATGTGTATGAGAAGAAGCTGAGGCCACCTTT 1557
QY 861 TAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGATGAAGAATTTACAGCTCA 920
Db 1558 CAAGCCCCAGGTCACTCTGAGACTGACACCAAGGTATTTTCGATGAGGAGTTCCACAGCTCA 1617
QY 921 GACTATTACAATAACACACCTGAAATAATGA 953
Db 1618 GATGATCACCATCAGCCGCCCTGATCAAGATGA 1650

Search completed: February 15, 2006, 09:30:20
Job time : 860 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 04:46:41 ; Search time 633 Seconds
(without alignments)
10297.108 Million cell updates/sec

Title: US-10-601-311-2

Perfect score: 978
Sequence: 1 tctacaaccatcataaaag.....atggtatggactgcatggac 978

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978	100.0	1440	3	Aaa62451 Human Akt
2	978	100.0	1440	3	Ab150839 Human Akt
3	978	100.0	1547	3	Aaa62450 Human Akt
4	978	100.0	1547	12	Adn71939 Human ser
5	978	100.0	1547	13	Adt99288 Human Akt
6	978	100.0	2367	3	Aac61592 DNA encod
7	978	100.0	2811	10	Adc26888 DNA encod
8	978	100.0	2811	13	Adq88265 Human 141
9	976.4	99.8	3285	3	Aac77341 Human ORF
10	949.8	97.1	1570	3	Aaa96637 DNA encod
11	949.8	97.1	1570	4	Aah79025 Human Akt
12	949.8	97.1	1570	4	Aaa89264 Human ser
13	949.8	97.1	1570	12	Adg85244 Human Chr
14	949.8	97.1	1703	14	Adz49363 Insulin s
15	604.2	61.8	2277	12	Adn71941 Chicken s
16	527	53.9	1722	13	Abd33334 Murine ca
17	527	53.9	1741	10	Adc26886 DNA encod
18	527	53.9	1741	12	Adp48781 Mouse Akt
19	527	53.9	3010	14	Adx01484 Human tol

20	525	53.7	1140	10	Adc26889	DNA encod
21	525	53.7	2626	3	Aaa09078	Wild type
22	525	53.7	2626	6	Aad28550	Mouse Akt
23	525	53.7	2626	10	Adc26885	DNA encod
24	525	53.7	2626	12	Adp48780	Mouse Akt
25	525	53.7	2626	14	Adx01483	Human tol
26	525	53.7	6891	12	Adl25356	ARK5 rela
27	517.4	52.9	1593	12	Adq84311	Human tum
28	517.4	52.9	1593	13	Adq86862	Human tum
29	517.4	52.9	1593	13	Adq83643	Human tum
30	517.4	52.9	1593	13	Adq85783	Human tum
31	517.4	52.9	1593	13	Acn40577	Tumour-as
32	517.4	52.9	2562	13	Abd33336	Human can
33	515.8	52.7	1446	6	Ab150838	Human Akt
34	515.8	52.7	1599	2	Aat71252	Mouse Akt
35	515.8	52.7	1599	3	Aaa08448	Human Akt
36	515.8	52.7	1599	3	Aaz60814	Nucleotid
37	515.8	52.7	1599	10	Adc26887	DNA encod
38	515.8	52.7	1599	11	Adi31678	Human CDN
39	515.8	52.7	1599	12	Adn71937	Human pro
40	515.8	52.7	1599	13	Adh83745	Human lym
41	515.8	52.7	1715	6	Abv94263	Breast ca
42	515.8	52.7	1715	12	Adp48783	Human Akt
43	515.8	52.7	1715	14	Adz26090	Human gen
44	515.8	52.7	3897	13	Acn43263	Human dia
45	512.2	52.4	2729	14	Adx01463	Human tol

ALIGNMENTS

RESULT 1
AAA62451
ID AAA62451 standard; cDNA; 1440 BP.
XX
AC AAA62451;

DT 13-NOV-2000 (first entry)
XX

DE Human Akt-3 coding sequence.

XX Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytostatic;
KW apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
KW chromosome 1q43-44; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 1..1440
FT /tag= a
FT /product= "Akt-3"

XX WO200037613-A2.

XX PD 29-JUN-2000.

XX PF 17-DEC-1999; 99WO-GB004311.

XX PR 22-DEC-1998; 98GB-00028375.

XX PA (JANC) JANSEN PHARM NV.

XX PI Masure SLJ, Richardson A;

XX DR WPI; 2000-498840/44.

XX DR P-PSDB; ABL13393.

XX New human serine/threonine kinase protein and the polynucleotide encoding
PT the protein, useful for preparing a medicament for treating disorders
PT associated with human serine/threonine kinase protein activity,
PT especially cancer.

XX Claim 4; Fig 1; 61pp; English.

XX The present sequence is the coding region of the nucleotide sequence that
CC encodes human Akt-3. Akt-3 is a third human isoform of Akt, which is also
CC known as protein kinase B (PKB) or "related to A and C protein kinase"
CC (RAC-PK). The gene encoding Akt-3 is located on human chromosome 1,
CC region q43-q44. A human hippocampal EST sequence that showed high
CC similarity to the rat RAC-PKgamma sequence was used to design primers for
CC 3' rapid amplification of cDNA ends (3' RACE). The sequence obtained in
CC the first round of 3' RACE was used to design primers for a second round.
CC The complete sequence was then amplified from human hippocampal cDNA by
CC PCR using primers based on the product of the second round of 3' RACE.
CC Akt can inhibit apoptosis induced by detachment from the extracellular
CC matrix. The Akt-3 nucleic acid molecule and protein may be used as
CC medicaments for treating cancer. Agents which influence the activity of
CC Akt-3 protein, and so stimulate apoptosis, may also be used to treat
CC diseases associated with Akt-3
XX Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

SQ Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

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Query Match      100.0%; Score 978; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1.3e-257;
Matches 978; Conservative 0; Mismatches 0; Indels 0
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Qy	1	TCTACAA	CCCTCATATAA	AGAAAGACA	CAATGAATG	ATTTTGACT	ATTTTGAA	ACTACTAGGT	60		
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Qy	61	AAAGGC	ACTTTTGG	AAAGTTATTTT	TGGTTCG	AGAGAGG	CNAAGT	TGGAAATACTATGCT	120		
Db	466	AAAGGC	ACTTTTGG	AAAGTTATTTT	TGGTTCG	AGAGAGG	CNAAGT	TGGAAATACTATGCT	525		
Qy	121	ATGAAG	ATTCTGA	AGAAAGAGT	CATTATTC	CAAGAGG	ATGAAGT	TGGCACACACTCTAACT	180		
Db	526	ATGAAG	ATTCTGA	AGAAAGAGT	CATTATTC	CAAGAGG	ATGAAGT	TGGCACACACTCTAACT	585		
Qy	181	GAAGC	AGAGTATTTAA	AGAACAC	ATAGACAT	CCCTTTTTT	TAAACAT	CCCTTGGAAATATTCCTTC	240		
Db	586	GAAGC	AGAGTATTTAA	AGAACAC	ATAGACAT	CCCTTTTTT	TAAACAT	CCCTTGGAAATATTCCTTC	645		
Qy	241	CAGAC	AAAAAGCCG	TTTGTGTTT	TGTGATG	GAATATGTT	TAAATGGG	GGCGAGCTGTTTTTC	300		
Db	646	CAGAC	AAAAAGCCG	TTTGTGTTT	TGTGATG	GAATATGTT	TAAATGGG	GGCGAGCTGTTTTTC	705		
Qy	301	CATT	TGTCG	AGAGACG	GGTGCTCT	CTGAGAC	CGCACACG	TGTTCTATGGTGCGAGAAATT	360		
Db	706	CATT	TGTCG	AGAGACG	GGTGCTCT	CTGAGAC	CGCACACG	TGTTCTATGGTGCGAGAAATT	765		
Qy	361	GTCT	CTGCTT	GGACTACT	CTACATTC	CGGAAAG	ATTGTGTAC	CGGTGATCTCAAGTTGGAG	420		
Db	766	GTCT	CTGCTT	GGACTACT	CTACATTC	CGGAAAG	ATTGTGTAC	CGGTGATCTCAAGTTGGAG	825		
Qy	421	AATCT	AATGCT	TGGA	CAAGAT	TGGCCAC	ATAAAAA	TTACAGATTTTGGACTTTGCAAGAA	480		
Db	826	AATCT	AATGCT	TGGA	CAAGAT	TGGCCAC	ATAAAAA	TTACAGATTTTGGACTTTGCAAGAA	885		
Qy	481	GGG	ATCAG	ATG	CAGCC	ACCATGA	AGACATTCT	TGTGSCATCTCNGAATATCTGSCACCA	540		
Db	886	GGG	ATCAG	ATG	CAGCC	ACCATGA	AGACATTCT	TGTGSCATCTCNGAATATCTGSCACCA	945		
Qy	541	GAG	TGTTAG	AAGATA	TGACTAT	TGGCCG	CAGCTAG	ACTGGTGGGGCTTAGGGGTTGTC	600		
Db	946	GAG	TGTTAG	AAGATA	TGACTAT	TGGCCG	CAGCTAG	ACTGGTGGGGCTTAGGGGTTGTC	1005		
Qy	601	ATG	TATG	AAATG	ATGTGT	TGGAGG	TACTTTTCT	TACAAAC	CAGGACCATGAGAAACTTTTT	660	
Db	1006	ATG	TATG	AAATG	ATGTGT	TGGAGG	TACTTTTCT	TACAAAC	CAGGACCATGAGAAACTTTTT	1065	
Qy	661	GAAT	TTAAT	TTAA	TGGA	AGACATTTAA	ATTTTCT	CTCGAAC	ACTCTCTTT	CAGATGCAAAATCA	720
Db	1066	GAAT	TTAAT	TTAA	TGGA	AGACATTTAA	ATTTTCT	CTCGAAC	ACTCTCTTT	CAGATGCAAAATCA	1125
Qy	721	TTG	CTTCC	AGG	CTTGT	AT	AAAGAT	CCAAAT	TAAACG	CCCTTGTGTGGAGGACCGATGAT	780

transformed cells; (7) screening compounds for their ability to modify intracellular Akt activity by contact with cells expressing Akt or Hsp90; and (8) drug compositions containing antibodies recognizing the binding domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and Hsp90 have cytostatic, cardiant, vasotropic, hepatotropic, antidiabetic, neuroprotective and nootropic activities. Blockade of the binding of Hsp90 with Akt increases the sensitivity of cells to apoptosis induction. Akt and Hsp90 can be used in the prevention and treatment of diseases with which apoptosis regulation is associated, including cancer (such as gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and prostate cancer), diabetes, Alzheimer's disease, cell death caused by radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The present sequence encodes human Akt3 which is used in the exemplification of the present invention

XX Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

Query Match 100.0%; Score 978; DB 6; Length 1440;

Best Local Similarity 100.0%; Pred. No. 1.3e-257;

Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTACAAACCCATATAAAGAAAGACAATGAATGATTTTGACTATTGGAACCTACTAGGT 60
 DB |||||
 406 TCTACAAACCCATATAAAGAAAGACAATGAATGATTTTGACTATTGGAACCTACTAGGT 465
 QY 61 AAAGGACATTTGGGAAAGTATTGTTTCAGAGAAGCGAAGTGGAAATCTATGCT 120
 DB |||||
 466 AAAGGACATTTGGGAAAGTATTGTTTCAGAGAAGCGAAGTGGAAATCTATGCT 525
 QY 121 ATGAAGATTCTGAAGAAGCAAGTCATTATTGCAAAAGGATGAAGTGCACACACTCTAACT 180
 DB |||||
 526 ATGAAGATTCTGAAGAAGCAAGTCATTATTGCAAAAGGATGAAGTGCACACACTCTAACT 585
 QY 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATCTCTTC 240
 DB |||||
 586 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATCTCTTC 645
 QY 241 CAGACAAAGACCGTTTGTTGTTGTTGATGGAATATGTTAAATGGGGCGAGCTGTTTTC 300
 DB |||||
 646 CAGACAAAGACCGTTTGTTGTTGTTGATGGAATATGTTAAATGGGGCGAGCTGTTTTC 705
 QY 301 CATTTGTCGAGAGCGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT 360
 DB |||||
 706 CATTTGTCGAGAGCGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT 765
 QY 361 GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTGTACCGTATCTCAAGTTGGAG 420
 DB |||||
 766 GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTGTACCGTATCTCAAGTTGGAG 825
 QY 421 AATCTAATCTGGAACAAAGATGGCCACATAAAATTAAGATTTTGGACTTTGCAAAAGAA 480
 DB |||||
 826 AATCTAATCTGGAACAAAGATGGCCACATAAAATTAAGATTTTGGACTTTGCAAAAGAA 885
 QY 481 GGGATCAGAGTGCAGCCACCATGAAGACATCTGTGGCACTCCAGATATCTGGCACC 540
 DB |||||
 886 GGGATCAGAGTGCAGCCACCATGAAGACATCTGTGGCACTCCAGATATCTGGCACC 945
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 DB |||||
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 QY 601 ATGTATGAATGATGTGGGAGGTTTACCTTTCTCAACACGAGCATGAGAAACCTTTT 660
 DB |||||
 1006 ATGTATGAATGATGTGGGAGGTTTACCTTTCTCAACACGAGCATGAGAAACCTTTT 1065
 QY 661 GAATTAATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
 DB |||||
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 QY 721 TTGCTTTTCAGGCTCTTTGATAAAGGATCAAAATAACCGCTTTGGTGGAGGACCATGAT 780
 DB |||||
 1126 TTGCTTTTCAGGCTCTTTGATAAAGGATCAAAATAACCGCTTTGGTGGAGGACCATGAT 1185

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 1186 GCAAAAGAAATTTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1245
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 DB |||||
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 DB |||||
 1366 GGTATGGACTGCATGGAC 1383

RESULT 3
 AAA62450
 ID AAA62450 standard; cDNA; 1547 BP.
 XX AC AAA62450;
 XX DT 13-NOV-2000 (first entry)
 XX Human Akt-3 nucleotide sequence.
 DE Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytotostatic;
 KW apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
 KW chromosome 1q43-44; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH 11..1450
 CDS /*tag= a
 FT /product= "Akt-3"
 FT /note= "nucleotides 11 to 1447 are given as SEQ ID NO: 2
 FT in the specification and are specifically claimed in
 FT claim 4 (see AAA62451)"
 XX WO200037613-A2.
 XX 29-JUN-2000.
 XX 17-DEC-1999; 99WO-GB004311.
 XX 22-DEC-1998; 98GB-00028375.
 XX (JANC) JANSSEN PHARM NV.
 XX Masure SLJ, Richardson A;
 XX WPI: 2000-498840/44.
 XX P-PSDB; AAB13393.
 XX New human serine/threonine kinase protein and the polynucleotide encoding
 PT the protein, useful for preparing a medicament for treating disorders
 PT associated with human serine/threonine kinase protein activity,
 PT especially cancer.
 XX Claim 3; Fig 1; 61pp; English.
 XX The present sequence encodes human Akt-3. Akt-3 is a third human isoform
 CC of Akt, which is also known as protein kinase B (PKB) or "related to A
 CC and C protein kinase" (RAC-PK). The gene encoding Akt-3 is located on
 CC human chromosome 1, region q43-q44. A human hippocampal EST sequence that
 CC showed high similarity to the rat RAC-PKgamma sequence was used to design
 CC primers for 3' rapid amplification of cDNA ends (3' RACE). The sequence
 CC obtained in the first round of 3' RACE was used to design primers for a
 CC second round. The complete sequence was then amplified from human
 CC hippocampal cDNA by PCR using primers based on the product of the second
 CC round of 3' RACE. Akt can inhibit apoptosis induced by detachment from

CC the extracellular matrix. The Akt-3 nucleic acid molecule and protein may
CC be used as medicaments for treating cancer. Agents which influence the
CC activity of Akt-3 protein, and so stimulate apoptosis, may also be used
CC to treat diseases associated with Akt-3

XX
SQ Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;

Query Match 100.0%; Score 978; DB 3; Length 1547;
Best Local Similarity 100.0%; Pred. No. 1.4e-257;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTACAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTGAAACTACTAGGT 60
Db 416 TCTACAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTGAAACTACTAGGT 475
Qy 61 AAAGGCACCTTTTGGGAAAGTTATTGTTGTCGAGAGAGGCAAGTGGAAATATCTATGCT 120
Db 476 AAAGGCACCTTTTGGGAAAGTTATTGTTGTCGAGAGAGGCAAGTGGAAATATCTATGCT 535
Qy 121 ATGAAGATTCTGAAGAAAGAGTCAATATTGCAAGAGATGAAGTGGCACACACTCTAACT 180
Db 536 ATGAAGATTCTGAAGAAAGAGTCAATATTGCAAGAGATGAAGTGGCACACACTCTAACT 595
Qy 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240
Db 596 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 655
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 300
Db 656 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 715
Qy 301 CATTTGTCGAGAGCGGCTTCTCTGAGGACCGCACACACTTTTCTATGGTGACAGAAAT 360
Db 716 CATTTGTCGAGAGCGGCTTCTCTGAGGACCGCACACACTTTTCTATGGTGACAGAAAT 775
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTAACGTGATCTCAAGTTGGAG 420
Db 776 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTAACGTGATCTCAAGTTGGAG 835
Qy 421 AATCTAATGCTGGACAAGATGGCCACATAAANAATACAGATTTTGACATTTGCAAGAA 480
Db 836 AATCTAATGCTGGACAAGATGGCCACATAAANAATACAGATTTTGACATTTGCAAGAA 895
Qy 481 GGGATCAGATGCGAGCCACCACATGAAGACATTTCTGTGCACTCCAGAAATATCTGGCACCA 540
Db 896 GGGATCAGATGCGAGCCACCACATGAAGACATTTCTGTGCACTCCAGAAATATCTGGCACCA 955
Qy 541 GAGGTGTTGAAGATAATGACTATGGCGGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db 956 GAGGTGTTGAAGATAATGACTATGGCGGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015
Qy 601 ATGTATGAAATGATGTGGGAGGTTACCTTTCTACACACGAGGACCATGAGAACTTTTT 660
Db 1016 ATGTATGAAATGATGTGGGAGGTTACCTTTCTACACACGAGGACCATGAGAACTTTTT 1075
Qy 661 GAAATTAATTAATGAAGACATTAATAATTTCTCTGCAACACTCTCTTCAGATGCAAAATCA 720
Db 1076 GAAATTAATTAATGAAGACATTAATAATTTCTCTGCAACACTCTCTTCAGATGCAAAATCA 1135
Qy 721 TTGCTTTTCAGGCTCTTGATAAAGATCCAAATAAAGCCCTTGTGTGGAGGACCAAGATGAT 780
Db 1136 TTGCTTTTCAGGCTCTTGATAAAGATCCAAATAAAGCCCTTGTGTGGAGGACCAAGATGAT 1195
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTTCTCTGAGTAACTGGCAAGATGTATATGAT 840
Db 1196 GCAAAAGAAATATGAGACACAGTTTCTTCTCTGAGTAACTGGCAAGATGTATATGAT 1255
Qy 841 AAAAGGCTTGTAACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 900
Db 1256 AAAAGGCTTGTAACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 1315
Qy 901 GATGAAGATTTAAGCTCAGCTATTTACAATAACACACCTGAAATATGATGAGGAT 960
XX

Db 1316 GATGAAGATTTTACAGCTCAGACTATTTACAATAACACCACCTGAAAAATATGATGAGGAT 1375
Qy 961 GGTATGGACTGCATGGAC 978
Db 1376 GGTATGGACTGCATGGAC 1393
RESULT 4
ADN71939
ID ADN71939 standard; cDNA; 1547 BP.
XX
AC ADN71939;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human serine/threonine kinase Akt-3 encoding cDNA SEQ ID NO:25.
XX
KW kinase pathway inhibitor; anti-prostate cancer;
KW mitogen-activated protein kinase pathway inhibitor;
KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase pathway;
KW PI3K/Akt kinase pathway; cytosolic; MAP kinase inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
KW human; serine/threonine kinase Akt-3; chromosome 1; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 11..1450
FT /tag= a
FT /product= "serine/threonine kinase Akt-3"
XX
PN W02004041185-A2.
XX
PD 21-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-US034636.
XX
XX 31-OCT-2002; 2002US-0423340P.
XX
XX (UYRP) UNIV ROCHESTER.
XX
XX Chang C, Lee Y, Lin W;
XX
XX WPI; 2004-390508/36.
XX
XX P-PSDB; ADN71940.
XX
XX Composition useful in the treatment of e.g. prostate cancer comprises a
XX kinase pathway inhibitor and an anti-prostate cancer compound.
XX
XX Disclosure; SEQ ID NO 25; 118pp; English.
XX
XX The present invention describes a composition (C1) which comprises a
XX kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
XX Also described: (1) identification of a mitogen-activated protein (MAP)
XX kinase pathway inhibitor involving incubating an antiandrogen or a
XX library of molecules with a cell containing an activable MAP kinase
XX pathway and selecting the molecules which inhibit the activation of the
XX MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
XX involving incubating a cell with hydroxyflutamide and potential
XX inhibitor, and assaying the level of activation of MAP kinase pathway or
XX phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
XX cytosolic activity, and can be used as a MAP kinase inhibitor.
XX phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
XX receptor (AR) inhibitor. C1 can be used in the treatment of prostate
XX cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
XX prostate cancer inhibitor; and for reducing the number of prostate cancer
XX cells in a sample. The composition C1 provides effective combination
XX therapy as compared to prior therapies. The present sequence encodes
XX human serine/threonine kinase Akt-3, which is used in the exemplification
XX of the present invention.

SQ	Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;	
Query Match	100.0%; Score 978; DB 12; Length 1547;	
Best Local Similarity	100.0%; Pred. No. 1.4e-257;	
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 TCTACACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 60	
DB	416 TCTACACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 475	
QY	61 AAAGGCACCTTTTGGGAAAGTATTTTGGTTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 120	
DB	476 AAAGGCACCTTTTGGGAAAGTATTTTGGTTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 535	
QY	121 ATGAAGATTCTGAAGAAAGAAAGTCAATTAATTCGAAAGGATGAAGTGGCACACACTCTAACT 180	
DB	536 ATGAAGATTCTGAAGAAAGAAAGTCAATTAATTCGAAAGGATGAAGTGGCACACACTCTAACT 595	
QY	181 GAAAGCAGAGTATTAAAGNACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 240	
DB	596 GAAAGCAGAGTATTAAAGNACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 655	
QY	241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300	
DB	656 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 715	
QY	301 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTCGAGAAATT 360	
DB	716 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTCGAGAAATT 775	
QY	361 GTCTCTGCCCTTGCACTATCTACATTCGGAAGATGTGTACCGTGATCTCAAGTTGGAG 420	
DB	776 GTCTCTGCCCTTGCACTATCTACATTCGGAAGATGTGTACCGTGATCTCAAGTTGGAG 835	
QY	421 AATCTAAATCTCGACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480	
DB	836 AATCTAAATCTCGACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 895	
QY	481 GGGATCACAGATGCGACCCACCAATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540	
DB	896 GGGATCACAGATGCGACCCACCAATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 955	
QY	541 GAGGTGTTAGAAGATAATGACTATGCGCAGCAGTAGACTGTGGGGCCTAGGGGTTGTCT 600	
DB	956 GAGGTGTTAGAAGATAATGACTATGCGCAGCAGTAGACTGTGGGGCCTAGGGGTTGTCT 1015	
QY	601 ATGTATGAATCATGTGTGGGAGGTTTACCTTTCTACACCAGGACCATGAGAACTTTT 660	
DB	1016 ATGTATGAATCATGTGTGGGAGGTTTACCTTTCTACACCAGGACCATGAGAACTTTT 1075	
QY	661 GAATTAATATTAAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720	
DB	1076 GAATTAATATTAAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1135	
QY	721 TTGCTTTTACGGGCTTTGTATAAGGATCCAAATAAACCGCTTGGTGGAGGACCATGAT 780	
DB	1136 TTGCTTTTACGGGCTTTGTATAAGGATCCAAATAAACCGCTTGGTGGAGGACCATGAT 1195	
QY	781 GCAAAAGAAATATTAGACACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840	
DB	1196 GCAAAAGAAATATTAGACACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1255	
QY	841 AAAAGCTTTGTACCTCTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT 900	
DB	1256 AAAAGCTTTGTACCTCTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTT 1315	
QY	901 GATGAAGAAATTTACAGCTCAGACTATTACAATAACACCACTGAAATAATGATGAGGAT 960	
DB	1316 GATGAAGAAATTTACAGCTCAGACTATTACAATAACACCACTGAAATAATGATGAGGAT 1375	
QY	961 GGTATGGAATGCAATGGAC 978	
DB	1376 GGTATGGAATGCAATGGAC 1393	

RESULT 5	
ADT9288	
ID	ADT9288 standard; cDNA; 1547 BP.
XX	
AC	ADT9288;
XX	
DT	13-JAN-2005 (first entry)
XX	
DE	Human Akt3 cDNA.
XX	
KW	Akt3; Akt3 inhibitor; tumour; cancers; atherosclerosis; psoriasis;
KW	autoimmune diseases; bacterial infection; viral infection; HIV infection;
KW	hepatitis; antiarteriosclerotic; antibacterial; anti-HIV;
KW	antiinflammatory; antiproliferative; cytostatic; hepatocytic;
KW	immunosuppressive; virucide; human; protein kinase B; ss.
XX	
OS	Homo sapiens.
XX	
PN	US6809194-B1.
XX	
PD	26-OCT-2004.
XX	
PF	08-MAY-2001; 2001US-00851670.
XX	
PR	10-MAY-2000; 2000US-0203543P.
XX	
PA	(CHIR) CHIRON CORP.
XX	
PI	Reinhard C, Jefferson AB;
XX	
DR	WPI; 2004-755774/74.
XX	
PT	New Akt3 inhibitor, useful for treating cancer, atherosclerosis,
XX	psoriasis, autoimmune diseases, and bacterial and viral infections.
PS	Example 1; SEQ ID NO 1; 23pp; English.
XX	
CC	The present invention relates to an Akt3 inhibitor, where the inhibitor
CC	is an antisense molecule capable of inhibiting the expression of human
CC	Akt3. The Akt3 inhibitor is useful for preparing a medicament for
CC	modulating cell proliferation and for treating tumours, cancers,
CC	atherosclerosis, psoriasis, autoimmune diseases, bacterial infections and
CC	viral infections like human immunodeficiency virus 1 (HIV) infections or
CC	hepatitis. The present sequence is the human Akt3 cDNA. Akt3 is also
CC	known as protein kinase B.
XX	
SQ	Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;
Query Match	100.0%; Score 978; DB 13; Length 1547;
Best Local Similarity	100.0%; Pred. No. 1.4e-257;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TCTACACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 60
DB	416 TCTACACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 475
QY	61 AAAGGCACCTTTTGGGAAAGTATTTTGGTTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 120
DB	476 AAAGGCACCTTTTGGGAAAGTATTTTGGTTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 535
QY	121 ATGAAGATTCTGAAGAAAGAAAGTCAATTAATTCGAAAGGATGAAGTGGCACACACTCTAACT 180
DB	536 ATGAAGATTCTGAAGAAAGAAAGTCAATTAATTCGAAAGGATGAAGTGGCACACACTCTAACT 595
QY	181 GAAACAGAGTATTAAAGNACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 240
DB	596 GAAACAGAGTATTAAAGNACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 655
QY	241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300
DB	656 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 715

Qy 301 CATTGTGCGAGAGCGGGTGTCTCTGAGAGCGCACACCGTTTCTATGTCGAGAAATT 360
Db |||||||
Qy 716 CATTGTGCGAGAGCGGGTGTCTCTGAGAGCGCACACCGTTTCTATGTCGAGAAATT 775
Db |||||||
Qy 361 GTCTCTGCGTGGACTATCTACATTCGGAAGAAAGTTGTGTACCGTGATCTCAAGTTGGAG 420
Db |||||||
Qy 776 GTCTCTGCGTGGACTATCTACATTCGGAAGAAAGTTGTGTACCGTGATCTCAAGTTGGAG 835
Qy 421 AATCTAATGCTGGACAAGATGGCCACATAAAATTTACAGATTTTGACATTTGCAGAA 480
Db |||||||
Qy 836 AATCTAATGCTGGACAAGATGGCCACATAAAATTTACAGATTTTGACATTTGCAGAA 895
Qy 481 GGGATCACAGATGCGAGCCACCACCAATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 540
Db |||||||
Qy 896 GGGATCACAGATGCGAGCCACCACCAATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 955
Qy 541 GAGGTGTTGAAGATAATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db |||||||
Qy 956 GAGGTGTTGAAGATAATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015
Qy 601 ATGTATGAATGATGTGGGAGGTACCTTTCTACCAACGAGGACCATGAGAACTTTT 660
Db |||||||
Qy 1016 ATGTATGAATGATGTGGGAGGTACCTTTCTACCAACGAGGACCATGAGAACTTTT 1075
Qy 661 GAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db |||||||
Qy 1076 GAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1135
Qy 721 TTGCTTTTCAGGGCTCTTGATAAAGATGCAAAATTAACGCCCTTGTTGGAGGACGAGATGAT 780
Db |||||||
Qy 1136 TTGCTTTTCAGGGCTCTTGATAAAGATGCAAAATTAACGCCCTTGTTGGAGGACGAGATGAT 1195
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAAACTGCGAAGATGTATATGAT 840
Db |||||||
Qy 1196 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAAACTGCGAAGATGTATATGAT 1255
Qy 841 AAAAAGCTTGTAACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTT 900
Db |||||||
Qy 1256 AAAAGCTTGTAACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTT 1315
Qy 901 GATGAAGAAATTAAGCTCAGCTAGATTAATACATAACACACCTGAAAAATATGATGAGAT 960
Db |||||||
Qy 1316 GATGAAGAAATTAAGCTCAGCTAGATTAATACATAACACACCTGAAAAATATGATGAGAT 1375
Qy 961 GGTATGACTGCATGGAC 978
Db |||||||
Qy 1376 GGTATGACTGCATGGAC 1393

RESULT 6
AAC61592
ID AAC61592 standard; DNA; 2367 BP.
XX AC AAC61592;
XX AC AAC61592;
DT 19-FEB-2001 (first entry)
XX DNA encoding a human kinase B-gamma polypeptide.
DE
XX Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;
KW phosphoinositide 3-kinase; insulin signalling;
KW pleckstrin homology domain; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT 10..1449
FT CDS /*tag= a
FT /product= "kinase B-gamma polypeptide"
XX
XX WO200058446-A1.
XX

PD 05-OCT-2000.
XX
PF 23-MAR-2000; 2000WO-SB000571.
XX
PR 25-MAR-1999; 99SE-00001115.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Attersand A;
XX
XX WPI; 2000-647230/62.
DR P-PSDB; AAB19284.
XX
XX Novel human protein kinase B gamma polynucleotides and polypeptides
PT useful as probe or primers in polymerase chain reaction and to raise
PT antibodies useful in diagnostic assays for detecting polypeptide
PT expression.
XX
XX Claim 1; Page 16-19; 27pp; English.
XX
CC The present sequence encodes a human protein kinase B gamma (PKB)
CC polypeptide. PKB is activated by insulin or insulin growth factor 1.
CC Lipid products of phosphoinositide 3-kinase act in insulin signaling by
CC binding to pleckstrin homology domains of PKB. PKB polynucleotides may be
CC used as a source of probes and primers. PKB polypeptides are used to
CC raise antibodies, which are used in diagnostic assays. The polypeptides
CC are also useful for screening for compounds which affect insulin
CC signalling pathways
XX
SQ Sequence 2367 BP; 752 A; 444 C; 514 G; 657 T; 0 U; 0 Other;
Query Match 100.0%; Score 978; DB 3; Length 2367;
Best Local Similarity 100.0%; Pred. No. 1.6e-257;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCTACACCCATCATAAAGAAAGACAATGAATGATTTTGACTATTGAAACTACTAGGT 60
Db |||||||
Qy 415 TCTACACCCATCATAAAGAAAGACAATGAATGATTTTGACTATTGAAACTACTAGGT 474
Qy 61 AAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 120
Db |||||||
Qy 475 AAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 534
Qy 121 ATGAAGATTCTGAAGAAAGAAAGTCATTATTGCAAGGATGAAGTGGCACACACTTAAC 180
Db |||||||
Qy 535 ATGAAGATTCTGAAGAAAGAAAGTCATTATTGCAAGGATGAAGTGGCACACACTTAAC 594
Qy 181 GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC 240
Db |||||||
Qy 595 GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC 654
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300
Db |||||||
Qy 655 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 714
Qy 301 CATTTGTGCGAGAGAGCGGGTGTCTCTCGAGGACCGCACAGCTTTCTATGTCGAGAAATT 360
Db |||||||
Qy 715 CATTTGTGCGAGAGAGCGGGTGTCTCTCGAGGACCGCACAGCTTTCTATGTCGAGAAATT 774
Qy 361 GTCTCTGCGTGGACTATCTACATTCGGAAGAAAGTTGTGTACCGTGATCTCAAGTTGGAG 420
Db |||||||
Qy 775 GTCTCTGCGTGGACTATCTACATTCGGAAGAAAGTTGTGTACCGTGATCTCAAGTTGGAG 834
Qy 421 AATCTAATGCTGGACAAGATGGCCACATAAAATTTACAGATTTTGACATTTTGCAAGAA 480
Db |||||||
Qy 835 AATCTAATGCTGGACAAGATGGCCACATAAAATTTACAGATTTTGACATTTTGCAAGAA 894
Qy 481 GGGATCACAGATGCGAGCCACCACCAATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 540
Db |||||||
Qy 895 GGGATCACAGATGCGAGCCACCACCAATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 954
Qy 541 GAGGTGTTGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db |||||||

Db 955 GAGGTGTTAGAGATAATGACTATATGCCGAGCAGTAGACTGCTGGGGCTAGGGTTGTC 1014
QY 601 ATGTATGAATAATGATGTGGAGGTTACTCTTCTCAACCCAGGACCATGAGAAACTTTT 660
Db 1015 ATGTATGAATAATGATGTGGAGGTTACTCTTCTCAACCCAGGACCATGAGAAACTTTT 1074
QY 661 GAATTAATAATTAATGAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db 1075 GAATTAATAATTAATGAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1134
QY 721 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAAGCTTTGGTGGAGCACCATGAT 780
Db 1135 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAAGCTTTGGTGGAGCACCATGAT 1194
QY 781 GCAAAAGAAATTAATGAGACATGTTCTTCTCTGAGGTAACCTGCGAAGATGATATGAT 840
Db 1195 GCAAAAGAAATTAATGAGACATGTTCTTCTCTGAGGTAACCTGCGAAGATGATATGAT 1254
QY 841 AAAAGCTGTGACCTCTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 900
Db 1255 AAAAGCTGTGACCTCTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 1314
QY 901 GATGAAGAAATTAATGAGACATGTTCTTCTCTGAGGTAACCTGCGAAGATGATATGAT 960
Db 1315 GATGAAGAAATTAATGAGACATGTTCTTCTCTGAGGTAACCTGCGAAGATGATATGAT 1374
QY 961 GGTATGGACTGCATGGAC 978
Db 1375 GGTATGGACTGCATGGAC 1392

RESULT 7

ADC26888
ID ADC26888 standard; DNA; 2811 BP.
XX
AC ADC26888;
XX
DT 18-DEC-2003 (first entry)
XX
DE DNA encoding human Akt3.
XX
KW ds; gene; Akt; human; apoptosis; myocardial infarction;
KW hyperproliferative disease; cancer; rheumatoid arthritis;
KW inflammatory bowel disease; osteoarthritis; leiomyoma; adenoma; lipoma;
KW haemangioma; fibroma; vascular occlusion; restenosis; atherosclerosis;
KW pre-neoplastic lesion; adenomatous hyperplasia;
KW prostatic intraepithelial neoplasia; carcinoma in situ;
KW oral hairy leukoplakia; psoriasis.
XX
OS Homo sapiens.
XX
PN US2003144204-A1.
XX
PD 31-JUL-2003.
XX
PF 19-DEC-2002; 2002US-00324985.
XX
PR 19-DEC-2001; 2001US-034215P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Spencer D;
XX
DR WPI; 2003-720709/68.
XX
PT New expression vector for modulating apoptosis or for treating myocardial
PT infarction or cancer, comprises an inducible chimeric protein that
PT comprises a mutant Akt polypeptide fused to a ligand-binding domain.
XX
PS Disclosure; SEQ ID NO 4; 38pp; English.
XX
CC The invention relates to an expression vector comprising an inducible
CC chimeric protein which comprises a mutant Akt polypeptide fused to a

CC ligand-binding domain. The composition and methods are useful in
CC modulating apoptosis or in treating myocardial infarction or
CC hyperproliferative diseases such as cancer, rheumatoid arthritis,
CC inflammatory bowel disease, osteoarthritis, leiomyomas, adenomas,
CC lipomas, haemangiomas, fibromas, vascular occlusion, restenosis,
CC atherosclerosis, pre-neoplastic lesions (e.g. adenomatous hyperplasia or
CC prostatic intraepithelial neoplasia), carcinoma in situ, oral hairy
CC leukoplakia or psoriasis. The present sequence represents DNA encoding
CC human Akt3.
XX
SQ Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;
Query Match 100.0%; Score 978; DB 10; Length 2811;
Best Local Similarity 100.0%; Pred. No. 1.7e-257;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTACAAACCCATCATATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGT 60
Db 406 TCTACAAACCCATCATATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGT 465
QY 61 AAAGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAACTATATGCT 120
Db 466 AAAGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAACTATATGCT 525
QY 121 ATGAAGATCTCGAAGAAAGAGTCAATTTTGCAGAGAGGCAAGTGGCAACACTCTAACT 180
Db 526 ATGAAGATCTCGAAGAAAGAGTCAATTTTGCAGAGAGGCAAGTGGCAACACTCTAACT 585
QY 181 GAAAGCAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATAATTCTCTTC 240
Db 586 GAAAGCAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATAATTCTCTTC 645
QY 241 CAGACAAAGAACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTC 300
Db 646 CAGACAAAGAACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTC 705
QY 301 CATTTGTCGAGAGCGGGGTGTTCTCTGAGNACCCACACACGTTTCTATGTCGAGAAATTT 360
Db 706 CATTTGTCGAGAGCGGGGTGTTCTCTGAGNACCCACACACGTTTCTATGTCGAGAAATTT 765
QY 361 GTCTCTGCTGGACTATCTACATTTCCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db 766 GTCTCTGCTGGACTATCTACATTTCCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 825
QY 421 AATCTAATGCTGGCAAGATGGCCACATAAATAATTAAGATTTTGGACTTTGCAAAAGAA 480
Db 826 AATCTAATGCTGGCAAGATGGCCACATAAATAATTAAGATTTTGGACTTTGCAAAAGAA 885
QY 481 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTCGACCTCCAGAAATATCTGGCACC 540
Db 886 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTCGACCTCCAGAAATATCTGGCACC 945
QY 541 GAGGTGTTAGAGATAATGACTATATGCCGAGCAGTAGACTGCTGGGGCTAGGGTTGTC 600
Db 946 GAGGTGTTAGAGATAATGACTATATGCCGAGCAGTAGACTGCTGGGGCTAGGGTTGTC 1005
QY 601 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACCCAGGACCATGAGAAACTTTT 660
Db 1006 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACCCAGGACCATGAGAAACTTTT 1065
QY 661 GAATTAATAATTAATGGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db 1066 GAATTAATAATTAATGGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1125
QY 721 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAAGCTTTGGTGGAGCACCATGAT 780
Db 1126 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAAGCTTTGGTGGAGCACCATGAT 1185
QY 781 GCAAAAGAAATTAATGAGACATGTTTCTTCTGAGGTAACCTGCGAAGATGATATGAT 840
Db 1186 GCAAAAGAAATTAATGAGACATGTTTCTTCTGAGGTAACCTGCGAAGATGATATGAT 1245
QY 841 AAAAGCTGTGACCTCTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 900

Db 1246 AAAAAGCTTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 1305
Qy 901 GATCAAGAAATTTACAGCTCAGACTATTACAAATACACACCTGAAAATATGATGAGGAT 960
Db 1306 GATGAAGAAATTTACAGCTCAGACTATTACAAATACACACCTGAAAATATGATGAGGAT 1365
Qy 961 GGTATGGAGCTCATGGAC 978
Db 1366 GGTATGGAGCTCATGGAC 1383
RESULT 8
ID ADQ88265
XX ADQ88265 standard; DNA; 2811 BP.
XX AC ADQ88265;
XX DT 21-OCT-2004 (first entry)
XX DE Human 14180 DNA encodes a rac gamma Ser/Thr protein kinase RAC-PK-gamma.
XX KW human; gene; ds; cardiovascular disorder; thrombotic disorder;
XX KW differential expression; gene therapy; aberrant vascularisation;
XX KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;
XX KW dyslipidaemia; high blood pressure; heart failure; cardiant;
XX KW thrombolytic; anticoagulant; antilipaeamic; hypotensive; cardiant;
XX KW rac gamma Ser/Thr protein kinase; RAC-PK-gamma.
XX OS Homo sapiens.
XX PN WO2004063340-A2.
XX PD 29-JUL-2004.
XX PF 13-JAN-2004; 2004WO-US000393.
XX PR 13-FEB-2003; 2003US-0439683P.
XX PR 05-FEB-2003; 2003US-0445216P.
XX PR 18-FEB-2003; 2003US-0448036P.
XX PR 12-MAR-2003; 2003US-0454189P.
XX PR 25-MAR-2003; 2003US-0457541P.
XX PR -29-APR-2003; 2003US-0466411P.
XX PR 08-MAY-2003; 2003US-0469041P.
XX PR 10-JUN-2003; 2003US-047414P.
XX PR 13-JUN-2003; 2003US-0478560P.
XX PR 24-JUL-2003; 2003US-0489772P.
XX PR 28-JUL-2003; 2003US-0490660P.
XX PR 03-SEP-2003; 2003US-0499838P.
XX PR 22-SEP-2003; 2003US-0504786P.
XX PR 24-SEP-2003; 2003US-0505570P.
XX PR 17-OCT-2003; 2003US-0512418P.
XX PR 27-OCT-2003; 2003US-0514660P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;
XX PI Rogrigne-Way A, Tomlinson JE;
XX DR WPI; 2004-553729/53.
XX DR P-ESDB; ADQ88266.
XX PT Identifying a compound for treating a cardiovascular or thrombotic
XX disorder by combining a compound to be tested with e.g., a 9380, 9462,
XX 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
XX and detecting the binding.
XX PS Claim 1; SEQ ID NO 107; 512pp; English.
XX CC This invention relates to a novel compound that is capable of treating a
XX cardiovascular or thrombotic disorder. Specifically, it refers to the
XX identification of nucleic acid molecules, and the encoded proteins
XX thereof, which are differentially expressed in cardiovascular disease

CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation,
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,
CC dyslipidaemia, high blood pressure or heart failure. As such, they
CC exhibit cardiant, thrombolytic, anticoagulant, antilipaeamic, hypotensive
CC and cardiant activities. This polynucleotide sequence is a human DNA
CC molecule that is differentially expressed in a patient with a
CC cardiovascular disorder, given in an exemplification of the invention.
XX SQ Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;
Query Match 100.0%; Score 978; DB 13; Length 2811;
Best Local Similarity 100.0%; Pred. No. 1.7e-257;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCTACAACCCATCATATAAAGAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT 60
Db 406 TCTACAACCCATCATATAAAGAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT 465
Qy 61 AAAGGCACCTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAATATCTATGCT 120
Db 466 AAAGGCACCTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAATATCTATGCT 525
Qy 121 ATGNAGATCTGAAGAAAGAGTCAATTTATTTGCAAGAGATGAGTGGGCACACACTTAACT 180
Db 526 ATGAAGATCTGAAGAAAGAGTCAATTTATTTGCAAGAGATGAGTGGGCACACACTTAACT 585
Qy 181 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCTTTGAAATATTTCCCTTC 240
Db 586 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCTTTGAAATATTTCCCTTC 645
Qy 241 CAGACAAAAGACCGTTTGT 300
Db 646 CAGACAAAAGACCGTTTGT 705
Qy 301 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATT 360
Db 706 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATT 765
Qy 361 GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db 766 GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 825
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAGAA 480
Db 826 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTACAGATTTTGGACTTTGCAAGAA 885
Qy 481 GGGATCAAGATGCGAGCCACCATGAACACATTTCTGTGGCACTCCAGATATATCTGGACCA 540
Db 886 GGGATCAAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGATATATCTGGACCA 945
Qy 541 GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCTTAGGGGTTGTC 600
Db 946 GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCTTAGGGGTTGTC 1005
Qy 601 ATGTATCAAAATGATGTGGGAGGTTTACCTTTTCAACACGAGACCATAGAGAACTTTTT 660
Db 1006 ATGTATCAAAATGATGTGGGAGGTTTACCTTTTCAACACGAGACCATAGAGAACTTTTT 1065
Qy 661 GAATTAATATTAATGGAAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db 1066 GAATTAATATTAATGGAAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA 1125
Qy 721 TTGCTTTTCAAGGCTCTTTGATAAAGATCCAAATAAAGCCCTTGGTGGAGGACCAAGATGAT 780
Db 1126 TTGCTTTTCAAGGCTCTTTGATAAAGATCCAAATAAAGCCCTTGGTGGAGGACCAAGATGAT 1185
Qy 781 GCAAAAGAAATATATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840

Qy 781 GCAAAAGAAATTATGAGACACAGTTTCTCTCTGAGTAAACTGGCAAGATGTATATGAT 840
Db 1660 GCAAAAGAAATTATGAGACACAGTTTCTCTCTGAGTAAACTGGCAAGATGTATATGAT 1719
Qy 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 900
Db 1720 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 1779
Qy 901 GATGAAGAATTATACAGTCTAGCTATTTACAACTCAAGTAACTCTGAGACAGATAGTATATTTT 960
Db 1780 GATGAAGAATTATACAGTCTAGCTATTTACAACTCAAGTAACTCTGAGACAGATAGTATATTTT 1839
Qy 961 GGTATGAGCTGCATGGAC 978
Db 1840 GGTATGAGCTGCATGGAC 1857

RESULT 10
ID AAA96637 standard; DNA; 1570 BP.

XX AAA96637;
AC
DT 08-FEB-2001 (first entry)
XX DNA encoding a human Akt3 polypeptide.

XX Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;
KW hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;
KW reperfusion injury; myocardial ischemia reperfusion injury; stroke;
KW liver damage; renal failure; organ transplantation; coronary artery; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 126..1523
FT FT /*tag= a
FT FT /product= "Akt3"

XX WO200056866-A2.

XX 28-SEP-2000.

XX 14-MAR-2000; 2000WO-US006574.

XX 19-MAR-1999; 99US-0125108P.

XX (AVET) AVENTIS PHARM PROD INC.

XX Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;

XX WPI; 2000-638260/61.

XX P-PSDB; AAB19011.

PT Novel AKT3 nucleic acid and proteins capable of preventing apoptotic cell
PT death induced by apoptosis stimulating kinase 1 useful for treating
PT myocardial infarction or ischemia reperfusion injury.

XX Claim 3; Page 62-64; 73pp; English.

XX The present sequence encodes a human Akt3 protein. Expression of Akt3
CC prevents apoptotic cell death induced by apoptotic stimulating kinase 1
CC (ASK1). The Akt3 polypeptide is useful for inhibiting cell death,
CC preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or
CC necrosis in a patient suffering from myocardial infarction or ischemia
CC reperfusion injury. The polypeptide is also useful for treating
CC myocardial infarction or ischemia reperfusion injury, where the
CC reperfusion injury is myocardial ischemia reperfusion injury or is
CC associated with stroke, liver damage, renal failure, organ
CC transplantation or coronary artery by pass grafting

XX Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Query Match 97.1%; Score 949.8; DB 3; Length 1570;
Best Local Similarity 99.8%; Pred. No. 7.5e-250;
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTACACCCTATCAATAAAGAGACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT 60
Db 531 TCTACACCCTATCAATAAAGAGACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT 590
Qy 61 AAAGGCACTTTTGGGAAAGTTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGTCT 120
Db 591 AAAGGCACTTTTGGGAAAGTTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGTCT 650
Qy 121 ATGAAGATTCTGAAGAAAGAGTCAATTATTTGCAAAAGGATGAAGTGGCACACACTCTAACT 180
Db 651 ATGAAGATTCTGAAGAAAGAGTCAATTATTTGCAAAAGGATGAAGTGGCACACACTCTAACT 710
Qy 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTTGAATAATTCCTTC 240
Db 711 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTTGAATAATTCCTTC 770
Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGSAATATGTTAATGGGGCGAGCTGTTTTTC 300
Db 771 CAGACAAAAGACCGTTTGTGTTTGTGATGSAATATGTTAATGGGGCGAGCTGTTTTTC 830
Qy 301 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGSGTGCAGAAATT 360
Db 831 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGSGTGCAGAAATT 890
Qy 361 GTCTCTCCCTTGGACTATCTACATTCGGAAAGATTGTGACCGTGATCTCAAGTTGGAG 420
Db 891 GTCTCTCCCTTGGACTATCTACATTCGGAAAGATTGTGACCGTGATCTCAAGTTGGAG 950
Qy 421 AATCTAATGCTGGCAAAAGATGGCCACATAAATAATTACAGATTTTGACATTTTGCAAGAA 480
Db 951 AATCTAATGCTGGCAAAAGATGGCCACATAAATAATTACAGATTTTGACATTTTGCAAGAA 1010
Qy 481 GGGATCACAGATGCAGCCACCATGAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 1011 GGGATCACAGATGCAGCCACCATGAGACATTTCTGTGSCATCCAGAAATATCTGGCACCA 1070
Qy 541 GAGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCCTAGGGGTTGTC 600
Db 1071 GAGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCCTAGGGGTTGTC 1130
Qy 601 ATGTATGAATGATGTGTGGAGGTTTACCTTTCTACAAACAGGACCATGAGAAAATCTTTT 660
Db 1131 ATGTATGAATGATGTGTGGAGGTTTACCTTTCTACAAACAGGACCATGAGAAAATCTTTT 1190
Qy 661 GAATTAATATTAATGGAAGACATTTAAATTTTCTCGAACACTCTCTCAGATGCAAAATCA 720
Db 1191 GAATTAATATTAATGGAAGACATTTAAATTTTCTCGAACACTCTCTCAGATGCAAAATCA 1250
Qy 721 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACAGATGAT 780
Db 1251 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACAGATGAT 1310
Qy 781 GCAAAAGAAATTTATGACACACAGTTTCTCTCTGGAGTAAACTGGCAGATGTATATGAT 840
Db 1311 GCAAAAGAAATTTATGACACACAGTTTCTCTCTGGAGTAAACTGGCAGATGTATATGAT 1370
Qy 841 AAAAGGCTGTACCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 900
Db 1371 AAAAGGCTGTACCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 1430
Qy 901 GATGAAGAATTTACAGCTCAGCTATTTTACAAATAACACACCTGGAATAATATGA 953
Db 1431 GATGAAGAATTTACAGCTCAGCTATTTTACAAATAACACACCTGGAATAATATGA 1483

RESULT 11
AAH79025 standard; cDNA; 1570 BP.
XX

AC	AAH79025;	QY	1	TCTACACCCATCATAAAGAAAGCAATGAATGATTTTGGTCTGAGAGAGGCAAGTGGGAAATATCTATGCT	60
XX		DB	531	TTCTACACCCATCATAAAGAAAGCAATGAATGATTTTGGTCTGAGAGAGGCAAGTGGGAAATATCTATGCT	590
DE	Human Akt3 encoding cDNA SEQ ID NO 1.	QY	61	AAAGGCACCTTTTGGGAAAGTTATTTTGGTCTGAGAGAGGCAAGTGGGAAATATCTATGCT	120
KW	Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;	DB	591	AAAGGCACCTTTTGGGAAAGTTATTTTGGTCTGAGAGAGGCAAGTGGGAAATATCTATGCT	650
KW	cerebroprotective; neurotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;	QY	121	ATGAAGATTCTTGAAGAAAGAGTCAATTAATTCGAAAGGATGAAGTGGGCAACACTCTAACT	180
KW	osteopathic; vasotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;	DB	651	ATGAAGATTCTTGAAGAAAGAGTCAATTAATTCGAAAGGATGAAGTGGGCAACACTCTAACT	710
KW	apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;	QY	181	GAAAGCAGATTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC	240
KW	ischaemia reperfusion injury; stroke; organ transplantation;	DB	711	GAAAGCAGATTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC	770
KW	coronary artery bypass; tumour cell survival; gene therapy;	QY	241	CAGACAAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGGGGAGCTGTTTTTC	300
XX	Alzheimer's disease; Osteoarthritis; ss.	DB	771	CAGACAAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGGGGAGCTGTTTTTC	830
OS	Homo sapiens.	QY	301	CATTTGTCGAGAGCGGGTGTCTCTGAGGACCCACACACGTTTCTATGGTGCAGAAAT	360
XX		DB	831	CATTTGTCGAGAGCGGGTGTCTCTGAGGACCCACACACGTTTCTATGGTGCAGAAAT	890
XX		QY	361	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGTCTCAAGTTGGAG	420
XX		DB	891	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGTCTCAAGTTGGAG	950
XX		QY	421	AATCTAATGCTGGCAAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTTGGCAAGAA	480
XX		DB	951	AATCTAATGCTGGCAAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTTGGCAAGAA	1010
XX		QY	481	GGGATCACAGATGCGACCCACCATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA	540
XX		DB	1011	GGGATCACAGATGCGACCCACCATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA	1070
XX		QY	541	GAGGTGTTAGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCCCTAGGGGTGTC	600
XX		DB	1071	GAGGTGTTAGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCCCTAGGGGTGTC	1130
XX		QY	601	ATGTATGAAATGATGTGTGGGAGTTTACTCTTCTACACCCAGGACCATGAGAAATCTTTT	660
XX		DB	1131	ATGTATGAAATGATGTGTGGGAGTTTACTCTTCTACACCCAGGACCATGAGAAATCTTTT	1190
XX		QY	661	GAAATTAATTAATTAATGAAGACATTAATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA	720
XX		DB	1191	GAAATTAATTAATTAATGAAGACATTAATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA	1250
XX		QY	721	TTGCTTTTCAGGGCTCTTGATTAAGGATCAATAAATTAACCGCTTGGTGGAGGACAGATGAT	780
XX		DB	1251	TTGCTTTTCAGGGCTCTTGATTAAGGATCAATAAATTAACCGCTTGGTGGAGGACAGATGAT	1310
XX		QY	781	GCAAGAAATTTATGAGACACAGATTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	840
XX		DB	1311	GCAAGAAATTTATGAGACACAGATTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	1370
XX		QY	841	AAAAAGCTTTGACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT	900
XX		DB	1371	AAAAAGCTTTGACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT	1430
XX		QY	901	GATGAAGATTTTACAGCTCAGACTATTAATTAATTAACCAACCTGGAATAATATGA	953
XX		DB	1431	GATGAAGATTTTACAGCTCAGACTATTAATTAATTAACCAACCTGGAATAATATGA	1483
XX		RESULT 12			
XX		AAA89264			
XX		ID	AAA89264	standard; cDNA; 1570 BP.	
XX		XX	AAA89264;		
XX		AC	AAA89264;		
XX		DT	28-MAR-2001	(first entry)	

AAH79025;

31-JAN-2002 (first entry)

Human Akt3 encoding cDNA SEQ ID NO 1.

Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt; cerebroprotective; neurotrophic; hepatotrophic; inhibitor of apoptosis; ASK1; osteopathic; vasotrophic; hepatotrophic; inhibitor of apoptosis; ASK1; apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction; ischaemia reperfusion injury; stroke; organ transplantation; coronary artery bypass; tumour cell survival; gene therapy; Alzheimer's disease; Osteoarthritis; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 126..1523

/*tag= a

/product= "Akt3"

WO200168850-A2.

20-SEP-2001.

09-MAR-2001; 2001WO-US007663.

14-MAR-2000; 2000US-00526043.

(AVET) AVENTIS PHARM PROD INC.

Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;

WPI; 2001-582452/65.

P-PSDB; AAG78018.

New nucleic acid encoding human Akt3 protein, useful for inhibiting cell death and treating myocardial infarction, ischemia reperfusion injury associated with stroke, liver damage and renal failure.

Claim 1; Page 59-62; 73pp; English.

The invention relates to human Akt3 protein (AH/PH-domain containing serine/threonine kinase, Akt) comprising a fully defined sequence (AAG78018) of 465 amino acids, its splice variant or allelic variant, where the encoding polynucleotide hybridizes under stringent conditions with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570 base pairs defined in the specification. Akt3 has cerebroprotective, neurotrophic, neuroprotective, antiarthritic, osteopathic, vasotrophic and hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a regulatory region is useful for inhibiting cell death in cardiac myocytes resulting from hypoxia, apoptosis or necrosis and for treating myocardial infarction or ischaemia reperfusion injury, particularly that associated with stroke, liver damage, renal failure, organ transplantation or coronary artery bypass grafting. Agonist of Akt3 are useful for improving Akt3 activity during treatment of patients suffering from myocardial infarction or ischaemia reperfusion injury and inhibitors of Akt3 activity decrease tumour cell survival and result in tumour regression. Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the quantity of cell death and final infarct size, resulting in improved post-infarction function, improved quality of life and reduced mortality. In patients with existing heart failure, gene therapy with Akt3 retards the process of ventricular dilation and slows down disease progression. Akt3 gene therapy is useful for treating other disease states, involving cell death by apoptosis, including Alzheimer's disease, liver degeneration or osteoarthritis

Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Query Match 97.1%; Score 949.8; DB 4; Length 1570;

Best Local Similarity 99.8%; Pred. No. 7.5e-250;

Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX DE Human serine/threonine protein kinase Akt3 cDNA.
XX KW Akt3; human; protein kinase; vascular endothelial growth factor; VEGF;
KW inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; gene therapy;
KW ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 126..1523
XX FT /*tag= a
XX PN WO20007190-A2.
XX PD 21-DEC-2000.
XX PF 01-JUN-2000; 2000WO-US015098.
XX PR 11-JUN-1999; 99US-0138724P.
XX PR 03-NOV-1999; 99GB-00026058.
XX PA (AVET) AVENTIS PHARM PROD INC.
XX PI Guo K, Ivashchenko Y, Clark K;
XX DR WPI; 2001-025336/03.
XX DR P-PSDB; AAB19996.
XX PT Inducing expression of vascular endothelial growth factor, useful for
PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal
PT ischemia or pulmonary ischemia, comprises administering a
PT serine/threonine protein kinase Akt protein.
XX PS Example 1; Page 55-58; 67pp; English.
XX CC The present sequence is that of cDNA coding for human Akt3 (see
CC AAB19996), a novel Akt isoform. Akt3 is a serine/threonine protein kinase
CC capable of inducing vascular endothelial growth factor (VEGF) expression.
CC The sequence was deduced from 2 cDNA clones isolated from a human heart
CC cDNA library using a human Akt3 partial clone as probe. Akt3 is shorter
CC than Akt1 (see AAB1997) and Akt2 (see AAB19998) and there is no
CC significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of
CC the molecules. A claimed method of inducing expression of VEGF in a cell
CC involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding
CC such a protein. The cell is preferably from a patient suffering from an
CC ischaemic condition, especially cerebrovascular, renal, pulmonary, limb
CC or myocardial ischaemia, or ischaemic, idiopathic or hypertrophic
CC cardiomyopathy. The result is beneficial collateral blood vessel
CC formation. A claimed method of inhibiting angiogenesis in a patient
CC suffering from a tumour, comprises inhibiting the level of Akt activity
CC in the patient, thereby inhibiting production of VEGF. The method
CC comprises introducing an Akt antisense nucleic acid, an intracellular
CC binding protein (e.g. a scfv) that specifically binds the Akt protein, or
CC a nucleic acid encoding a dominant negative form of an Akt
XX SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Query Match 97.1%; Score 949.8; DB 4; Length 1570;
Best Local Similarity 99.8%; Pred. No. 7.5e-250;
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTACACCCCATATAAGAGACCAATGATGATTGCTATTGGAACCTACTAGGT 60
Db |||||
Qy 531 TCTACACCCCATATAAGAGACCAATGATGATTGCTATTGGAACCTACTAGGT 590
Db |||||
Qy 61 AAAGGCATTTTGGGAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120
Db |||||
Qy 591 AAAGGCATTTTGGGAAGTTATTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 650
Db |||||
Qy 121 ATGAAGATCTGAAGAGAGTCAATTTTCGAAGGATGAAGTGGCACACCTCTAACT 180
Db |||||
Qy 651 ATGAAGATCTGAAGAGAGTCAATTTTCGAAGGATGAAGTGGCACACCTCTAACT 710
Db |||||

Qy 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240
Db |||||
Qy 711 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 770
Db |||||
Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300
Db |||||
Qy 301 CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTT 360
Db |||||
Qy 831 CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATTT 890
Db |||||
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGTATCTCAAGTTGGAG 420
Db |||||
Qy 891 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGTATCTCAAGTTGGAG 950
Db |||||
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTGCAAGAA 480
Db |||||
Qy 951 AATCTAATGCTGGACAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTGCAAGAA 1010
Db |||||
Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGATATCTGGCACCA 540
Db |||||
Qy 1011 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGATATCTGGCACCA 1070
Db |||||
Qy 541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db |||||
Qy 1071 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1130
Db |||||
Qy 601 ATGTATGAATGATGTGGAGGTTACCTTTCTACAAACGAGGACCATGAGAAATCTTTTT 660
Db |||||
Qy 1131 ATGTATGAATGATGTGGAGGTTACCTTTCTACAAACGAGGACCATGAGAAATCTTTTT 1190
Db |||||
Qy 661 GAATTAATATTAATGGAAGACATTAATTTCTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db |||||
Qy 1191 GAATTAATATTAATGGAAGACATTAATTTCTCTCGAACACTCTCTTCAGATGCAAAATCA 1250
Db |||||
Qy 721 TTGCTTTTCAAGGCTCTTGATAAAGGATCCAAATAAAGCGCTTGGTGGAGGACCAAGATGAT 780
Db |||||
Qy 1251 TTGCTTTTCAAGGCTCTTGATAAAGGATCCAAATAAAGCGCTTGGTGGAGGACCAAGATGAT 1310
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Qy 781 GCAAAAGAAATATGAGACACAGTTTCTTCTCGAGTAAACCTGGCAAGATGTTATATGAT 840
Db |||||
Qy 1311 GCAAAAGAAATATGAGACACAGTTTCTTCTCGAGTAAACCTGGCAAGATGTTATATGAT 1370
Db |||||
Qy 841 AAAAGGCTTGTACTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATCTAGATATTTT 900
Db |||||
Qy 1371 AAAAGGCTTGTACTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATCTAGATATTTT 1430
Db |||||
Qy 901 GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGA 953
Db |||||
Qy 1431 GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGA 1483
Db |||||

RESULT 13
ADG85244
ID ADG85244 standard; DNA; 1570 BP.
XX AC ADG85244;
XX DT 25-MAR-2004 (first entry)
XX OS Human Chrysosporium associated DNA.
XX KW ds; gene; beta-glucosidic bond; beta-xylosidic bond; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 126..1523
XX FT /*tag= a
XX FT /product= "Chrysosporium associated protein"

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01-JAN-2004.
21-MAR-2003; 2003US-00394568.
06-OCT-1998; 98WO-BP006496.
06-OCT-1999; 99WO-NL000618.
13-APR-2000; 2000US-00548938.
(EMAL/) EMALFARB M A.
(BURL/) BURLINGAME R P.
(OLSO/) OLSON P T.
(SINI/) SINITSYN A P.
(PARR/) PARRICHE M.
(BOUS/) BOUSSON J C.
(PYNN/) PYNNONEN C M.
(PUNT/) PUNT P J.
(VZEI/) VAN ZEIJL C M J.
PI Emalfarb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parriche M;
PI Bousson JC, Pynnönen CM, Punt PJ, Van Zeijl CMJ;
DR WPI: 2004-061663/06.
DR P-PSDB; ADG85245.
XX Novel mutant Chryso sporium strain comprising nucleic acid sequence
PT encoding polypeptide of interest such as proteases and lipases, the
PT nucleic acid sequence being operably linked to expression-regulating
PT region.
XX Disclosure; SEQ ID NO 1; 70pp; English.
XX The invention relates to a mutant Chryso sporium strain comprising a
CC nucleic acid sequence encoding a polypeptide of interest. A mutant
CC Chryso sporium strain is useful for producing a polypeptide of interest by
CC culturing a mutant Chryso sporium strain under conditions permitting
CC expression of the protein or polypeptide, and recovering the subsequently
CC produced polypeptide of interest. The conditions further permit secretion
CC of the protein or polypeptide of interest. The polypeptides are useful
CC for hydrolysing beta-glucosidic bonds. A polypeptide is useful for
CC hydrolysing beta-xylosidic bonds. The present sequence represents human
CC Chryso sporium associated DNA.
XX
SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;
Query Match 97.1%; Score 949.8; DB 12; Length 1570;
Best Local Similarity 99.8%; Pred. No. 7.5e-250;
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCTCTTC 240
DB 711 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCTCTTC 770
QY 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTC 300
DB 771 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTC 830
QY 301 CATTTCTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCAGAAATT 360
DB 831 CATTTCTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCAGAAATT 890

QY 361 GTCTCTGCTTGGACTATCTACATTTCCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
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QY 421 AATCTAATGCTGGACAAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCAAAAGAA 480
DB 951 AATCTAATGCTGGACAAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCAAAAGAA 1010
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DB 1011 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 1070
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DB 1071 GAGGTGTTAGAAAGATAATGACTATGCGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTGTC 1130
QY 601 ATGTATGAAATGATGTGTGGGAGGTTTACCTTTCTACAACCCAGGACCATGAGAAACTTTTT 660
DB 1131 ATGTATGAAATGATGTGTGGGAGGTTTACCTTTCTACAACCCAGGACCATGAGAAACTTTTT 1190
QY 661 GAATTAATATTAATGGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
DB 1191 GAATTAATATTAATGGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1250
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QY 781 GCAAAAGAAATTTATGAGACACAGATTTCTCTCTGAGTAAACTGGCAAGATGTATATGAT 840
DB 1311 GCAAAAGAAATTTATGAGACACAGATTTCTCTCTGAGTAAACTGGCAAGATGTATATGAT 1370
QY 841 AAAAGCTTTGACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 900
DB 1371 AAAAGCTTTGACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 1430
QY 901 GATGAAGAATTTACAGCTCAGCTCAGCTATTAATAAACAACCACTGAAATAATGA 953
DB 1431 GATGAAGAATTTTACAGCTCAGCTCAGCTATTAATAAACAACCACTGAAATAATGTCA 1483
RESULT 14
ADZ49363
ID ADZ49363 standard; DNA; 1703 BP.
XX AC ADZ49363;
XX DT 30-JUN-2005 (first entry)
XX DE Insulin signaling pathway related gene, SEQ ID 692.
XX KW Antidiabetic; Gene Therapy; Non-insulin dependent diabetes;
XX KW insulin resistance; gene; ds.
XX OS Homo sapiens.
XX PN US2005085436-A1.
XX PD 21-APR-2005.
XX PF 08-JUL-2004; 2004US-00887553.
XX PR 08-JUL-2003; 2003US-0485883P.
XX PA (LIEH/) LI H.
XX PA (MAJU/) MA J.
XX PI Li H, Ma J;
XX DR WPI; 2005-305194/31.
XX PT Treating, preventing or ameliorating pathological conditions associated

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 05:12:42 ; Search time 3879 Seconds
(without alignments)
11796.279 Million cell updates/sec

Title: US-10-601-311-2

Perfect score: 978

Sequence: 1 tctacaaccatcataaaag.....atggtatggactgatgcac 978

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	890	91.0	1440	10	AV399351	AV399351 Homo sapi
3	818	83.6	1394	10	AV399353	AV399353 Mus muscu
4	783	80.1	967	5	BUS20318	BUS20318 AGENCOURT
5	705.8	72.2	785	5	CA430499	CA430499 UI-H-FHI-
6	696.8	71.2	766	5	BU703964	BU703964 UI-M-FOO-
7	685.8	70.1	777	7	CV557292	CV557292 UI-M-H2O-
8	670	68.5	703	3	BI917703	BI917703 603183679
9	646.4	66.1	656	6	CA867933	CA867933 ir83c04.y
10	635	64.9	641	6	CD875747	CD875747 f827d11.y
11	613.2	62.7	673	7	CN459710	CN459710 UI-M-HB0-
12	603.6	61.7	691	6	CF741213	CF741213 UI-M-GH0-
13	598.8	61.2	675	5	BU055259	BU055259 UI-M-FOO-
14	594	60.7	594	5	BU790247	BU790247 in52e10.x
15	593.8	60.7	710	7	CNS26605	CNS26605 UI-M-HN0-
16	590	60.3	590	7	CR854381	CR854381 DKFZp468P
17	586	59.9	586	6	CA943661	CA943661 ir83c04.x
18	572.6	58.5	783	6	CF723245	CF723245 UI-M-GV0-
19	566.6	57.9	667	6	CF532847	CF532847 UI-M-GH0-
20	565.2	57.8	630	6	CB247756	CB247756 UI-M-FI0-
21	557.6	57.0	820	6	CB520675	CB520675 UI-M-GI0-
22	552.4	56.5	669	7	CK640105	CK640105 UI-M-HN0-

23	547.4	56.0	1440	10	AY399352	AY399352 Pan trogl
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28	527	53.9	3724	4	AK028871	AK028871 Mus muscu
29	524	53.6	602	6	CB044389	CB044389 NISC GC04
30	522.8	53.5	675	7	CNS26012	CNS26012 UI-M-GI0-
31	518.2	53.0	651	6	CD351542	CD351542 UI-M-GI0-
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33	514.8	52.6	1659	11	DQ046227	DQ046227 Homo sapi
34	514.2	52.6	719	6	CA378893	CA378893 657877 NC
35	511.4	52.3	1654	11	DQ046228	DQ046228 Pan trogl
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37	505	51.6	1829	4	BC068106	BC068106 Danio rer
38	504.2	51.6	1848	4	AK040758	AK040758 Mus muscu
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41	488	49.9	1015	1	AL548951	AL548951 AL548951
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ALIGNMENTS

RESULT 1	HSM801048	1584 bp	mRNA	linear	HTC 16-APR-2005
LOCUS	HSM801048	1584 bp	mRNA	linear	HTC 16-APR-2005
DEFINITION	Homo sapiens mRNA; cDNA DKFZp434N0250 (from clone DKFZp434N0250).				
ACCESSION	AL117525				
VERSION	AL117525.1	GI:5912042			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1584)				
AUTHORS	Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Nehes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.				
CONSRTM	The German cDNA Consortium				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY				
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp434N0250) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434N0250 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.				
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ORIGIN

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Best Local Similarity	99.8%	Pred. No. 4.1e-245;		
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Db 619 AAAGCAGCTTTTGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACATGCT 678

Qy 121 ATGAAGATTCTGAAGAAGAAGTCATTATTGCAAAAGGATGAAGTGGCACACACTCTAACT 180

Db 679 ATGAAGATTCTGAAGAAGAAGTCATTATTGCAAAAGGATGAAGTGGCACACACTCTAACT 738

Qy 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAATCCTTGAATATTCCTTC 240

Db 739 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAATCCTTGAATATTCCTTC 798

Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC 300

Db 799 CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC 858

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Db 859 CATTGTGCGAGAGCGGGTCTCTCTGAGGACCGCACACAGTTTCTATGGTGCGAGAAATT 918

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Db 919 GTCTCTGCGCTTGGACTATCTACATTCGGAAGAAGTTGTACCGTGATCTCAAGTTGGAG 978

Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGACTTTGCAAAAGAA 480

Db 979 AATCTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGACTTTGCAAAAGAA 1038

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RESULT 2

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LOCUS Homo sapiens AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY399351

VERSION AY399351.1 GI:39755340

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1440)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1440)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

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Qy 61 AAAGGCATCTTTGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 120

Db 466 AAAGGCATCTTTGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 525

Qy 121 ATGAAGATTCGAGAAAGAAAGTCATTATTGCAAAAGGATGAAGTGGCACACACTCTAACT 180

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Db	946	GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCTAGGGGTTGTC	1005	
Qy	601	ATGTATGAAATGATGTGGGAGGTTTACCTTTCTACAAACGAGACCATGAGAAACTTTTT	660	
Db	1006	ATGTATGAAATGATGTGGGAGGTTTACCTTTCTACAAACGAGACCATGAGAAACTTTTT	1065	
Qy	661	GAATTAATTAATGGAAGACATTAATTTCTCGAAACATCTCTTTCAGATGCAAAATCA	720	
Db	1066	GAATTAATTAATGGAAGACATTAATTTCTCGAAACATCTCTTTCAGATGCAAAATCA	1125	
Qy	721	TGCTTTTCAAGGCTCTGATTAAGGATCCAAATAACGCTTGGTGGAGGACCATGAT	780	
Db	1126	TGCTTTTCAAGGCTCTGATTAAGGATCCAAATAACGCTTGGTGGAGGACCATGAT	1185	
Qy	781	GCAAAAGAAATTAATGAGACACAGTTTCTTCTCTGAGTAAACTGGCAAGATGATATGAT	840	
Db	1186	NN	1245	
Qy	841	AAAAAGCTGTACTCTTTTAAACCTCAAGTAAACATCTGAGACAGATCTAGATATTTT	900	
Db	1246	NNNNNNCTTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATCTAGATATTTT	1305	
Qy	901	GATGAAGATTTACAGCTCAGACTATTACATAACACCACTGAAATATATGATCAGGAT	960	
Db	1306	GATGAAGATTTACAGCTCAGACTATTACATAACACCACTGAAATATATGATCAGGAT	1365	
Qy	961	GGTATGGACTGCATGGAC	978	
Db	1366	GGTATGGACTGCATGGAC	1383	
RESULT 3				
LOCUS	AY399353	1394 bp	DNA	linear
DEFINITION	Mus musculus AKT3 gene, genomic survey sequence.			GSS 15-DEC-2003
ACCESSION	AY399353			
VERSION	AY399353.1			GI:39755342
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 1394)			
AUTHORS	Clark, A.G., Ghanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,			

Qy 661 GAATTAATATTAATGGAAGACATTAATAATTTCTCTCGAACACATCTCTTCTCAGATGCAAAATCA 720
Db 1020 GAAATTAATTAATGGAAGACATTAATAATTTCTCTCGAAGACATCTCTTCTCAGATGCAAAATCA 1079
Qy 721 TTGCTTTTCAGGCTCTTGATTAAGAGATCCAAATAAAGCCCTTGTGTGAGGACAGATGAT 780
Db 1080 TTGCTTTTCAGGCTCTTGATTAAGAGATCCAAATAAAGCCCTTGTGTGAGGACAGATGAT 1139
Qy 781 GCAAAAGAAATATGAGACACAGATTTCTTCTCTGAGTAAACTGCGAAGATGTATATGAT 840
Db 1140 NNN 1199
Qy 841 AAAAGCTTGTAACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACATGATATTTT 900
Db 1200 NNN 1259
Qy 901 GATCAAGAAATTTACAGCTCAGACTATTACATATACACACCTGAAATATGATGAGAT 960
Db 1260 GATCAAGAAATTTACAGCTCAGACTATTACATATACACACCTGAAATATGATGAGAT 1319
Qy 961 GGTATGGAATGCGATGGAC 978
Db 1320 GGCATGGACGCGATGGAC 1337

RESULT 4
BU520318 967 bp mRNA linear EST 12-SEP-2002
LOCUS AGENCOURT_10157385 NIH_MGC_134 Mus musculus cDNA clone
DEFINITION IMAGE:6518260 5', mRNA sequence.
ACCESSION BU520318
VERSION BU520318.1 GI:22827844
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 967)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM14099 Row: 1 Column: 05
High quality sequence start: 16
High quality sequence stop: 729.
Location/Qualifiers
1. 967
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6518260"
/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_134"
/notes="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
Cloned unidirectionally. Primer: Oligo dr. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC Library."

FEATURES

source
1. 967
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6518260"
/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_134"
/notes="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
Cloned unidirectionally. Primer: Oligo dr. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 80.1%; Score 783; DB 5; Length 967;
Best Local Similarity 93.4%; Pred. No. 4.2e-200;
Matches 883; Conservative 0; Mismatches 55; Indels 7; Gaps 6;

Qy 37 TTTGACTATTGTAAGCTACTAGGTAAAGGCATTTTGGGAAAGTATTTTGGTTGCGAG 96
Db 26 TTTGACTATTGTAAGCTACTAGG-AAAGGCATTTTGGGAAAG-TATTTTGGTTGCGAG 83
Qy 97 AAGCAAGTGGAAATATACTATGCTATGAAGATCTTGAAGAAGATCATTTTGGCAAG 156
Db 84 AAGCAAGTGGAAATATACTATGCTATGAAGATCTTGAAGAAGATCATTTTGGCAAG 143
Qy 157 GATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGAACACCTAGACATCCCTTT 216
Db 144 GATGAAGTGGCACACACTCTTACTGAAAGCAGAGTACTAAAGAACACACGACATCCATTT 203
Qy 217 TTAACATCTTTGAAATATTCCTTCCAGACAAAGACCGTTTGTGTGTTTGTGATGGAATAT 276
Db 204 TTAACATCTTTGAAATATTCCTTCCAGACAAAGACCGTTTGTGTGTTTGTGATGGAATAT 263
Qy 277 GTTAATGGGGCGGCGCTGTTTTCATTTCTCGAGAGCGGGTGTCTCTGAGGACCGC 336
Db 264 GTTAATGGCGGAGAGCTGTTTTCATTTCTCGAGAGCGAGTGTCTCTGAGGACCGC 323
Qy 337 ACAGCTTTCTATGCTGCGAGAAATTTGCTCTGCTTGGACTATCTACATTCGGGAAAGATT 396
Db 324 ACAGCTTTCTATGCTGCGAGAAATTTGCTCTGCTTGGACTATCTACATTCGGGAAAGATT 383
Qy 397 GTGTACCGTGATCTCAAGTTGGAGAAATCTTAATGCTGGACAAAGATGCCACATATAAAATT 456
Db 384 GTGTACCGTGATCTCAAGTTGGAGAAATTTGCTCTGCTTGGACTATCTACATTCGGGAAAGATT 443
Qy 457 ACAGATTTTGGACTTTGCAAGAAGGGATCACAGATGCAGCCACCATGAAGACATTTCTGT 516
Db 444 ACGGATTTTGGGCTTTTGCAGAAAGGGATCACAGATGCAGCTACCATGAAGACATTTCTGT 503
Qy 517 GSCATCCCAATATCTTGGCACAGAGGTCTTAGAAGATAATGACTATGCCGAGCAGTA 576
Db 504 GGCACACAGAGTACTTGGCACAGAGGTATTAGAGATAATGACTATGCCGAGCAGGTG 563
Qy 577 GACTGTGGGGCTTAGGGTGTGTCATGTATGAATGATGTGGGAGGTGTACCTTTCTAC 636
Db 564 GACTGTGGGGCTTAGGGTGTGTCATGTATGAATGATGTGGGAGGTGTACCTTTCTAC 623
Qy 637 AACGAGGACCATGAGAAATCTTTTGAATTAATTAATGAAGACATTAATTTCCCTCGA 696
Db 624 AACGAGGACCATGAGAAATCTTTTGAATTAATTAATGAAGACATTAATTTCCCTCGA 683
Qy 697 ACATCTCTTTCAGATGCAAAATCATTTGCTTTAGGGCTCTTGTATAAGGATCCAAATAAA 756
Db 684 ACATCTCTTTCAGATGCAAAATCATTTGCTTTAGGGCTCTTGTATAAGGATCCAAATAAA 741
Qy 757 CGCTTTGGTGGAGGACAGATGATGCAAAAGAAATTAAGACACAG-TTCTTTCTCTGG 815
Db 742 CGCTTTGGTGGAGGCGCAGATGATGCAAAAGAAATCATGAGGCATAGTTTTTTTCTGG 801
Qy 816 AGTAAACTGGCAAGATGTATGATGATAAGGCTGTACCTCTTTTAACTCAAGTAAC 875
Db 802 AGTAAACTGGCAAGATGTATGATGATAAGGCTGTACCTCTTTTAACTCAAGTAAC 861
Qy 876 ATCTGAGACAGATA-CTAGATATTTTGTGAAG-AAATTACAGCTCAGACTATTACATA 933
Db 862 ATCTGAAACAGACACCCCGATATTTTGTATGAAGAAATTTACAGCTCAGACTATTACATA 921
Qy 934 ACACCACTGAAATATATGATGAGGATGGTATGGACTGCAATGGAC 978
Db 922 ACACCACTGAAATATGACGACGCGCATGCGCGCATGGAC 966

RESULT 5
CA430499/c
LOCUS
DEFINITION UI-H-FHI-bft-c-24-0-UI.s1 NCI CGAP_FHI Homo sapiens cDNA clone
ACCESSION CA430499
VERSION CA430499.1 GI:24793225
KEYWORDS EST.

CA430499 785 bp mRNA linear EST 07-NOV-2002
UI-H-FHI-bft-c-24-0-UI.s1 NCI CGAP_FHI Homo sapiens cDNA clone
UI-H-FHI-bft-c-24-0-UI 3', mRNA sequence.
CA430499
CA430499.1 GI:24793225
EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 785)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue procurement: James Martin
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-42, sAT rich#Low complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

Location/Qualifiers
 1..785
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FH1-bft-c-24-0-UI"
 /tissue_type="Cell Line"
 /dev_stage="Adult"
 /lab_host="PH108 (Life Technologies)"
 /clone_lib="NCI-CGAP_FH1"
 /note="Organ: Chondrosarcoma; Vector: pTT73-Pac
 (Pharmacia) with a modified polylinker; Site 1: EcoR I;
 Site 2: Not I; NCI CGAP FH1 is a normalized cDNA library
 obtained from a cell line derived from grade I
 chondrosarcoma tissue. The library was constructed and
 normalized according to Bonaldo, Lennon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor,
 digested with Not I, and cloned directionally into
 pTT73-Pac vector. The oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 AGAATCCGGC. The cell line was provided by Dr. James Martin
 from the University of Iowa.
 TAG_ISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
 Chondrosarcoma
 TAG_LIB=UI-H-FH1
 TAG_SEQ=AGAATCCGGC"

ORIGIN
 Query Match 72.2%; Score 705.8; DB 6; Length 785;
 Best Local Similarity 99.3%; Pred. No. 2.9e-179;
 Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 242 AGACAAAGACCGTTGTGTTGTCATGGAATATGTTAATGGGGCGAGCTGTTTTC 301
 DB 785 AGACAAAGACCGTTGTGTTGTCATGGAATATGTTAATGGGGCGAGCTGTTTTC 726
 QY 302 ATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATTG 361
 DB 725 ATNTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATTG 666
 QY 362 TCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGA 421
 DB 665 TCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAGA 606
 QY 422 ATCTAATGCTGGCAAGATGGCCATATAAATATACAGATTTTGACATTTTGCAGAAAG 481
 DB 605 ATCTAATGCTGGCAAGATGGCCATATAAATATACAGATTTTGACATTTTGCAGAAAG 546

QY 482 CGATCAGATGCAGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAG 541
 DB 545 CGATCAGATGCAGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAG 486
 QY 542 AGGTGTTAGAAGATAATGACTATATGCGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTCA 601
 DB 485 AGGTGTTAGAAGATAATGACTATATGCGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTCA 426
 QY 602 TGTATGAAATGATGTGTGGAGGTTACTTCTTCAACACGAGACCATGAGAAACATTTTGG 661
 DB 425 TGTATGAAATGATGTGTGGAGGTTACTTCTTCAACACGAGACCATGAGAAACATTTTGG 366
 QY 662 AATTAATTAATGAAGACATTAATTTCTTCGAACTCTCTTCAGATGCABAATCAT 721
 DB 365 AATTAATTAATGAAGACATTAATTTCTTCGAACTCTCTTCAGATGCABAATCAT 306
 QY 722 TGCCTTACAGGGCTCTTGATAAAGGATCCAAATAAAGCGCTTGGTGGAGGACGAGATGATG 781
 DB 305 TGCCTTACAGGGCTCTTGATAAAGGATCCAAATAAAGCGCTTGGTGGAGGACGAGATGATG 246
 QY 782 CAAAAGAAATTAAGACACAGATTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATA 841
 DB 245 CAAAAGAAATTAAGACACAGATTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATA 186
 QY 842 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTTG 901
 DB 185 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTTG 126
 QY 902 ATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 953
 DB 125 ATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 74

RESULT 6
 BU703964
 LOCUS 766 bp mRNA linear EST 15-JUL-2003
 DEFINITION UI-M-F00-bzr-i-04-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone
 IMAGE:6406347 5', mRNA sequence.
 BU703964
 ACCESSION BU703964.1 GI:23631576
 VERSION BU703964.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 766)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue procurement: Dr. Jim Lin, University of Iowa
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1..766
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6406347"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="PH108 (T1 phage resistant)"

FEATURES
 source

/clone_lib="NIH_BMAP_F00"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
is TGAGAGAGCC. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match		71.2%;	Score 696.8;	DB 5;	Length 766;
Best Local Similarity		94.3%;	Pred. No. 7.7e-177;		
Matches 722;		Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0;
Qy	74	GGAAAGTATTTTGGTTCGAGAGAGCGCAAGTGGAAAATACTATGCTATGAGATTCTGA	133		
Db	1	GGGAAAGTATTTTGGTTCGAGAGAGCGCAAGTGGAAAATACTATGCTATGAGATTCTGA	60		
Qy	134	AGAAAGAGTCAATATTGCAAGAGTGAAGTGGCACACACTCTAACTGAAAGCAGAGTAT	193		
Db	61	AGAAAGAGTCAATATTGCAAGAGTGAAGTGGCACACACTCTTACTGAAAGCAGAGTAC	120		
Qy	194	TAAAGAACATAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTCCAGACAAAGACC	253		
Db	121	TAAAGAACACACAGACATCCATTTTAAACATCCTTTGAAATATTCCTTCCAGACAAAGACC	180		
Qy	254	GTTTGTGTTTTGATGGAATATGTTAATGGCGGAGAGCTTTTTCCATTTGTCGAGAG	313		
Db	181	GTTTGTGTTTTGATGGAATATGTTAATGGCGGAGAGCTTTTTCCATTTGTCGAGAG	240		
Qy	314	AGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGTGTGCAGAAATGTCTCTCCCTTGG	373		
Db	241	AGCGAGTGTCTCTGAGGACCGCACAGTTTCTATGTGTGCAGAAATGTCTCTCCTTTGG	300		
Qy	374	ACTATCTACATTCGGGAAAGATTGTGTACCTGTATCTCAAGTTGGAGAAATCAATGCTGG	433		
Db	301	ACTATCTACATTCGGGAAAGATTGTGTACCTGTATCTCAAGTTGGAGAAATTGATGCTAG	360		
Qy	434	ACAAGATGGCCACATATAAATTTACAGATTTTGGACCTTGGCAAGAGGGATCACAGATG	493		
Db	361	ATAAGGATGGCCATATAAATTTACGGATTTTGGGCTTTGCAAGAGGGGATCACAGATG	420		
Qy	494	CAGCCACCATGAAGACATCTCTGTGSCACTCCAGAAATATCTGGCACCGAGAGTGTAGAAG	553		
Db	421	CAGTACCATGAGACATCTCTGTGGCACACAGAGTACCTGGCACCGAGAGTATTAGAG	480		
Qy	554	ATAATGACTATGGCGGAGCAGTAGATGGTGGGCGCTAGGGGTTGTCTATGATGAATGA	613		
Db	481	ATAATGACTATGGCGGAGCAGTAGATGGTGGGCGCTAGGGTGTGTCTATGATGAATGA	540		
Qy	614	TGTGTGGAGGTTACCTTTCTACAAACGAGGCATGAGAAATCTTTTGAATTAATATTA	673		
Db	541	TGTGTGGAGGTTGCTTTCTACAAACGAGGCATGAGAAATCTTTTGAATTAATATTA	600		
Qy	674	TGGAGACATTAATTTTCTCGAACACCTCTCTCAGATGCAAAATCATTTGCTTTTCAGGGC	733		
Db	601	TGGAGACATTAATTTTCTCGAACACCTCTCTCAGATGCAAAATCATTTGCTTTTCAGGGC	660		
Qy	734	TCITTGATAAAGGATCCAAATAAAGCCCTTGTGGAGGACAGATGATGCAAAAGAAATTA	793		
Db	661	TCITTGATAAAGGATCCANATAAAGCCCTTGTGGAGGACAGATGATGCAAAAGAAATCA	720		
Qy	794	TGAGACACAGTTTCTCTCTGGAGTAAACTGGCAGATGTTATATGA	839		
pb	721	TGAGGCATAGTTTTTTTTCTGGAGTAAACTGGCAGATGTTATATGA	766		

RESULT 7

CV557292

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CV557292 777 bp mRNA linear EST 22-OCT-2004
UI-M-H20-csv-g-14-0-UI.r1 NIH_BMAP_H20 Mus musculus cDNA clone
IWAGB:30689725 5', mRNA sequence.
CV557292
CV557292.1 GI:54442702
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 777)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

Location/Qualifiers
1. 777
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/dev_stage="newborn 1,5,15 and embryos 15,16,17,18 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_H20"
/notes="Organ: Eye; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

ORIGIN

Query Match		70.1%;	Score 685.8;	DB 7;	Length 777;
Best Local Similarity		93.4%;	Pred. No. 7.2e-174;		
Matches 722;		Conservative 0;	Mismatches 50;	Indels 1;	Gaps 1;
Qy	107	GAAATATCTATGCTATGATGATGCTGAAGAAAGAGTCATTATTGCAAGGATGAAGTGG	166		
Db	6	GGAAATCTATGCTATGATGATGCTGAAGAAAGAGTCATTATTGCAAGGATGAAGTGG	64		
Qy	167	CACACACTTAAGTGAAGCGAGATATTAAGACACTAGACATCCCTTTTACATCCCT	226		
Db	65	CACACACTTACTGAAAGCAGAGTACTATAAGAACACACAGACATCCATCTTTTACATCCT	124		
Qy	227	TGAATATTTCTTCCAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGG	286		
Db	125	TGAATATTTCTTCCAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGG	184		


```
QY 287 GCGAGCTGTTTTCCATTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCT 346
Db 185 GAGAGCTGTTTTCCATTGTCGAGAGAGCGAGTGTCTCTGAGGACCGCACACGTTTCT 244
QY 347 ATGGTGCAGAAATGTCTCGCTTGGACTACTACATTCGCGAAAGATTGTGTACCGTG 406
Db 245 ATGGTGCAGAAATGTCTCGCTTGGACTACTACATTCGCGAAAGATTGTGTACCGTG 304
QY 407 ATCTCAAGTTGAGAAATCTAATGCTGGCAAAAGATGGCCACATATAAAATTACAGATTG 466
Db 305 ATCTCAAGTTGAGAAATTTGATGCTAGATAAGATGGCCATATAAAATTACGGAATTG 364
QY 467 GACTTTGCAAGAGGATACAGATGACAGATGCAGCCACCATGAAGACATTCGTGGCACTCCAG 526
Db 365 GCGTTTGCANAAGGATACAGATGACAGATGCAGCTTACCATGAAGACATTCGTGGCACACAG 424
QY 527 AATATCTGCGCACAGAGGTGTTAGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGG 586
Db 425 AGTACTGCGCACAGAGGTATTAGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGG 484
QY 587 GCCTAGGGTTGTCTATGTAAGAAATGATGTGGGAGGTTACTTTCTACAAACCGAGACC 646
Db 485 GCTTAGGTGTTGTCATGTAAGAAATGATGTGGGAGGTTGCTTTCTACAAACCGAGATC 544
QY 647 ATGAGAACTTTTGAATTAATTAATGAAGAGACATTAATTTCTCGAACACTCTCT 706
Db 545 ATGAGAACTTTTGAATTAATTAATGAAGAGACATTAATTTCTCGAAGCACTCTCT 604
QY 707 CAGATGCAAAATCAITTCCTTTGAGGCTCTTGATAAAGGATCCAAATAACCGCTTGGTG 766
Db 605 CAGATGCANAATCAITTCCTTTGAGGCTCTTGATAAAGGATCCAAATANACGCTTGGTG 664
QY 767 GAGGACCGAGATGCAAAAGAAATTAAGACACAGATTTCTCTCGAGTAAACTGGC 826
Db 665 GAGGCGCAGATGCAAAAGAAATCATGAGGCATAGTNTTTCTCGAGTANACTGGC 724
QY 827 AGATGCTATATGATAAAGCTTGACCTCTTTTAAACCTCAAGTAACATCT 879
Db 725 AGATGCTATATGATAAAGCTTGACCTCTTTTAAAGCTCAAGTAACATCT 777
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RESULT 8
LOCUS B1917703 703 bp mRNA linear EST 16-OCT-2001
DEFINITION 603183679F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5247930 5',
mRNA sequence.
ACCESSION B1917703
VERSION B1917703.1 GI:16181501
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 703)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11625 row: m column: 19
High quality sequence stop: 703.
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FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"

Source

1..703
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/mol_type="mRNA"

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/db_xref="taxon:9606"
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/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 68.5%; Score 670; DB 3; Length 703;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 692; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 278 TTAATGGGGGCGAGCTGTTTTCATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCA 337
Db 1 TTAATGGGGGCGAGCTGTTTTCATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCA 60
QY 338 CACGTTTCTATGGTGCAGAAATGTCTGCTGCTTGGACTATCTACATTCGCGAAAGATTG 397
Db 61 CACGTTTCTATGGTGCAGAAATGTCTGCTGCTTGGACTATCTACATTCGCGAAAGATTG 120
QY 398 TGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTCGACAAAGATGCCACATAAAATTA 457
Db 121 TGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTCGACAAAGATGCCACATAAAATTA 180
QY 458 CAGATTTTGGACTTTGCAAGAGAGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTG 517
Db 181 CAGATTTTGGACTTTGCAAGAGAGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTG 240
QY 518 GCATCTCCAGATATCTGGCACGAGAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAG 577
Db 241 GCATCTCCAGATATCTGGCACGAGAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAG 300
QY 578 ACTGTTGGGGCTAGGGGTGTGTCATGATGAATGATGTGGGAGGTACCTTTCTACA 637
Db 301 ACTGTTGGGGCTAGGGGTGTGTCATGATGAATGATGTGGGAGGTACCTTTCTACA 360
QY 638 ACCAGGACCATGAGAAACTTTTGAATTAATTAATGAGACACATTAATTTCTCTCGAA 697
Db 361 ACCAGGACCATGAGAAACTTTTGAATTAATTAATGAGACACATTAATTTCTCTCGAA 420
QY 698 CACTCTCTCAGATGCAAAATCATTTGCTTCAGGGCTCTTGATAAAGGATCCAAATAAAC 757
Db 421 CACTCTCTCAGATGCAAAATCATTTGCTTCAGGGCTCTTGATAAAGGATCCAAATAAAC 480
QY 758 GCCTTGGTGGAGGACACAGATGATGCAAAAGAAATTAATGAGACACAGTTTCTCTGGAG 817
Db 481 GCCTTGGTGGAGGACACAGATGATGCAAAAGAAATTAATGAGACACAGTTTCTCTGGAG 540
QY 818 TAAATCGCAAGATGATATATGATAAAGAGTTGTACCTCTCTTTTAAACCTCAAGTAACAT 877
Db 541 TAAATCGCAAGATGATATATGATAAAGAGTTGTACCTCTCTTTTAAACCTCAAGTAACAT 600
QY 878 CTGACACAGACTAGATATTTTGTAGAGAAATTTACAGCTCAGACTATTACATAACAC 937
Db 601 CTGACACAGACTAGATATTTTGTAGAGAAATTTTACAG-TCAGACTATTACATAACAC 659
QY 938 CACCTGAAAAATATCATGAGGATGTTATGGACTG 971
Db 660 CA-CTGAAAAATATCATGAGGATGTTATGGACTG 692

similar to TR:Q9Y243 Q9Y243 PROTEIN KINASE B GAMMA. ;, mRNA
sequence.

ACCESSION CA867933
VERSION CA867933.1 GI:27319482

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE

AUTHORS

1 (bases 1 to 656)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,
Williams, T., Jackson, Y., and Bowers, Y.

TITLE

JOURNAL

COMMENT

Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 486.

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608840"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 66.1%; Score 646.4; DB 6; Length 656;

Best Local Similarity 99.8%; Pred. No. 3e-163;

Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 211 CCCTTTTACATCCTTGAATATTCCTTCAGACAAAGACCGTTGCTTTGTGATG 270

Db 9 CGCTTTTAAACATCCTTGAATATTCCTTCAGACAAAGACCGTTGCTTTGTGATG 68

Qy 271 GAATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGCGGTGTTCTCTGAG 330

Db 69 GAATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGCGGTGTTCTCTGAG 128

Qy 331 GACCGCACACCTTTCTATGTCGAGAAATGTCCTGCTTGGACTATCTACATTCGCGA 390

Db 129 GACCGCACACCTTTCTATGTCGAGAAATGTCCTGCTTGGACTATCTACATTCGCGA 188

Qy 391 AAGATTGTGACCTGATCTCAAGTTGGAGATCTAATGCTGGCAAGATGGCCACATA 450

Db 189 AAGATTGTGACCTGATCTCAAGTTGGAGATCTAATGCTGGCAAGATGGCCACATA 248

Qy 451 AAAATTACAGATTTTGGACTTTGCAAAAGAGGGATCAAGATGAGCCACCATGAAGACA 510

Db 249 AAAATTACAGATTTTGGACTTTGCAAAAGAGGGATCAAGATGAGCCACCATGAAGACA 308

Qy 511 TTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAAATATAGCTATGGCGGA 570

Db 309 TTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAAATATAGCTATGGCGGA 368

Qy 571 GCAGTAGACTGGTGGGCGCTAGGGGTTGTCATGATGAAATGATGTGGGAGGTACCT 630

Db 369 GCAGTAGACTGGTGGGCGCTAGGGGTTGTCATGATGAAATGATGTGGGAGGTACCT 428

Qy 631 TTCTACAACAGGACCATGAGAAATCTTTTGAATTAATATTAATGGAAGACATTAATTT 690

Db 429 TTCTACAACAGGACCATGAGAAATCTTTTGAATTAATATTAATGGAAGACATTAATTT 488

Qy 691 CCTCGAACACTCTCTCAGATGCAAAATCAATGCTTTTCAGGGCTCTTGATAAAGATCCA 750

Db 489 CCTCGAACACTCTCTCAGATGCAAAATCAATGCTTTTCAGGGCTCTTGATAAAGATCCA 548

Qy 751 AATAAAGCGCTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGACACAGTTCTTC 810

Db 549 AATAAAGCGCTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGACACAGTTCTTC 608

Qy 811 TCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTTGACCTCT 858

Db 609 TCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTTGACCTCT 656

RESULT 10

LOCUS

CD675747 641 bp mRNA linear EST 24-JUN-2003
fa27dl1.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone
fa27dl1.5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

Wistow, G., Bernstein, S.L., Wyatt, M.K., Behal, A., Touchman, J.W.,
Bouffard, G., Smith, D. and Peterson, K.

TITLE

Expressed sequence tag analysis of adult human lens for the NEtBank
Project: over 2000 non-redundant transcripts, novel genes and
splice variants

JOURNAL

PUBMED

COMMENT

Contact: Wistow G
Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 27 row: d column: 11

Seq primer: M13RP1 reverse primer (ABI).

FEATURES

source

1..641
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/dev_stage="Adult"

/lab_host="EMDH10B"

/clone_lib="Human Lens cDNA (Normalized): fs"

/note="Organ: Eye; Vector: pCMVSPORT6; A human lens

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portion of double stranded plasmid DNA representing the

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368	CTAGATAAGGATGGCCATATAAAAATATACGATTTTGGCTTTTGCAGAAAGAGGATCA	427
490	GATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACGAGGTGTTA	549
428	GATGCAGCTACCATGAAGACATTTCTGTGGCACACACGAGTAGTACCTGGCACGAGGTATTA	487
550	GAAGATAATGACTATGGCCGAGCAGTAGACTGTGTGGGCGCTAGGGGTTGTCTATGTA	609
488	GAAGATAATGACTATGGCCGAGCCTGGACCTGTGTGGGCTTAGGTGTGTCTATGTA	547
610	ATGATGTGTGGGAGTTACCTTTCTACAAACGAGACCATGAGAAATCTTTTGAATTAATA	669
548	ATGATGTGTGGAAGTTGCCCTTTCTACAAACGAGCATGAGAAATCTTTTGAATTAATA	607
670	TTAATGGAAGACATTAATTTCTCGGAACATCTCTCTCAGATGCAAAATCATTTGCTTTCA	729
608	CTAATGGAAGACATTAATTTCCCGCAACATCTCTCTCAGATGCAAAATCATTTGCTTTCA	667
730	GGGGCTC 735	
668	GGGGCTC 673	
RESULT 12		
CF741213		
LOCUS	CF741213	
DEFINITION	UI-M-GHO- <i>cli-c-19-0-UI-r1</i> NIH_BMAP_GHO Mus musculus cDNA clone IMAGE:130618210 5', mRNA sequence.	
ACCESSION	CF741213	
VERSION	CF741213.1	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 691)	
TITLE	NTH-MSC http://mgc.nci.nih.gov/ .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgabbs-remail.nih.gov	
	Tissue Procurement: Dr. James Lin, University of Iowa	
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa	
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa	
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
	Clone Distribution: Distribution information can be found at	
	http://genome.uiowa.edu/distribution/mousef1.html	
	This clone was contributed by the Brain Molecular Anatomy Project (BMAP)	

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."									
ORIGIN									
Query Match	61.7%	Score	603.6;	DB	6;	Length	691;		
Best Local Similarity	94.6%;	Pred. No.	1.1e-151;						
Matches	646;	Conservative	0;	Mismatches	35;	Indels	2;	Gaps	2
QY	1	TC	TAC	ACC	CCAT	CAT	AAA	GAC	AAAGACACAAATGAATTTTGACTATT
DB	11	TC	TAC	ACC	CCAT	CAT	AAA	GAC	AAAGACACAAATGAATTTTGACTATT
QY	61	AA	AGG	CAC	TTTTGGG	AAAGTTAT	TTTTGGTT	CGAGAGAAAGGCAAGTGGAAAA	
DB	71	AA	AGG	-AC	TTTTGGG	AAAGTTAT	TTTTGGTT	CGAGAGAAAGGCAAGTGGAAAA	
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DB	130	AT	GAA	GAT	CTG	AAAGAAAGT	CATTAT	TGCAAAAGGATGAAGTGGCACAC	
QY	181	GA	AG	CAG	AGTAT	TAA	GRACA	CTAGACATCCCTTTTAA	
DB	190	GA	AA	G	CAG	AGTAT	TAA	GRACA	
QY	241	CAG	ACAAA	GAC	CGTTGTG	TTGTG	TATG	TATGTA	
DB	250	CAG	ACAAA	GAC	CGTTGTG	TTGTG	TATG	TATGTA	
QY	301	CAT	TTG	TG	CAG	AG	CGGGTGT	CTCTG	
DB	310	CAT	TTG	TG	CAG	AG	CGGGTGT	CTCTG	
QY	361	GT	CT	CG	CTT	GG	ACTAT	CTACAT	
DB	370	GT	CT	CG	CTT	GG	ACTAT	CTACAT	
QY	421	AA	TCT	TAAT	TG	CTG	CA	AAAGAT	
DB	430	AA	TCT	TAAT	TG	CTG	CA	AAAGAT	
QY	481	GG	GAT	CA	CAG	AT	CG	ACC	
DB	490	GG	GAT	CA	CAG	AT	CG	ACC	
QY	541	GAG	GT	TGA	AG	ATA	TG	ACT	
DB	550	GAG	GT	TGA	AG	ATA	TG	ACT	
QY	601	AT	CT	AT	GAA	TG	AT	G	
DB	610	AT	CT	AT	GAA	TG	AT	G	
QY	661	GA	ATT	TAAT	TAT	TAA	TGA	AGACAT	
DB	669	GA	ATT	TAAT	TAT	TAA	TGA	AGACAT	
RESULT	13								
LOCUS	BU055259								
DEFINITION	UT-M-FOO-bzp-j-23-0-UI.r1 NIH_BMAP_F00 Mus musculus CDNA clone								
ACCESSION	BU055259								
VERSION	BU055259.1								
KEYWORDS	EST.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
REFERENCE	1								
LOCUS	BU055259	675 bp	mRNA	linear	EST	26-AUG-2000			
DEFINITION	UT-M-FOO-bzp-j-23-0-UI.r1 NIH_BMAP_F00 Mus musculus CDNA clone								
ACCESSION	BU055259								
VERSION	BU055259.1								
KEYWORDS	EST.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
REFERENCE	1								

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgpbbs-remail.nih.gov
 Tissue procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
Seq primer: pYX-5.
Location/Qualifiers
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 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6405622"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH-BMAP_F00"
 /note="Organ: Brain; Vector: pYX-Asc; Site: 1: EcoR I;
 Site 2: Not I; The library was constructed according
 to Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TCAGAGACCC. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 61.2%; Score 598.8; DB 5; Length 675;
Best Local Similarity 94.8%; Pred. No. 2.2e-150;
Matches 640; Conservative 0; Mismatches 33; Indels 2; Gaps 2;

Qy 1 TCTACACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTCGAACTACTAGT 60
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 Db 3 TCTACACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTCGAACTACTAGT 62
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Qy 61 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120
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 Db 63 AAAGGCACCTTTTGGGAAA-TTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT 121
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Qy 121 ATGAAGATCTGAAGAAAGAGTCAATTATGCAAAAGGATGAAGTGGCCACACCTTAAT 180
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Qy 181 GAAAGCAGAGTATTAAGACACACTAGACATCCCTTTTAAATCCCTTCAATATTCCTTC 240
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Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTATGGGGCGAGCTGTTTTTC 300
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Qy 301 CATTTGTCCAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAT 360
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 Db 302 CATTTGTCCAGAGACGGAGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAT 361
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Qy 361 GTCTCTGCTTGGACTATCTACATTTCCGAAAGATTGTGACCGTATCTCAAGTTGGAG 420
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Db 362 GTCTCTGCTTGGACTATCTACATTTCTGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 421
 Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480
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 Qy 541 GAGGTGTTAGAAAGATAATGACTATATGGCCGACAGTAGACTGTGTGGGCTTGGGCTTGTTC 600
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 Qy 661 GAATTAATATTAATG 675
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 Db 661 GAATTAATATTAATG 675

RESULT 14
BU790247/c

LOCUS BU790247
DEFINITION in52e10.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6125683 3', similar to TR:Q9Y243 Q9Y243 PROTEIN KINASE B GAMMA. ;, mRNA

ACCESSION

BU790247

VERSION

BU790247.1 GI:23840478

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 594)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Bitter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishevili, R., Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoe@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 439.

FEATURES

source

1. .594
 /organism="Homo sapiens"
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 /clone="IMAGE:6125683"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
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Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

```

Query Match      60.7%; Score 594; DB 5; Length 594;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 366 TGCCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTATCTCAAGTTGGAGAAATCT 425
Db 594 TGCCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTATCTCAAGTTGGAGAAATCT 535

Qy 426 AATGCTCGACAAAGATGCCACATATAAAATACAGATTTTGGACTTTGCCAAGNAGGGAT 485
Db 534 AATGCTCGACAAAGATGCCACATATAAAATACAGATTTTGGACTTTGCCAAGNAGGGAT 475

Qy 486 CACAGATGCAGCCACCACCAATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAGAGGT 545
Db 474 CACAGATGCAGCCACCACCAATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAGAGGT 415

Qy 546 GTTAGAAGATAATGACTATATGCCGAGCAGTAGACTGTGTGGGGCTAGGGGTGTGTCATGTA 605
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Qy 606 TGAATGATGTGGGAGGTACCTTTCTACMACCAGGACCATCAGAAATCTTTTGAAT 665
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Qy 846 GCTTGTACCTCTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTGATGA 905
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RESULT 15

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CN526605
LOCUS      710 bp mRNA linear EST 29-APR-2004
DEFINITION UT-M-HN0-cou-n-06-00-11 NIH BMAP_HN0 Mus musculus CDNA clone
IMAGE:30650717 5', mRNA sequence.

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CN526605
VERSION    1
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus

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ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 710)

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NIH-MGC http://mgi.nci.nih.gov/.

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National Institutes of Health, Mammalian Gene Collection (MGC)

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Unpublished (1999)

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Contact: Robert Strausberg, Ph.D.

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Email: rcgaps@remail.nih.gov

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Tissue Procurement: Dr. James Lin University of Iowa

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CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

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CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html> This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. 710

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30650717"

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/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_HN0"

/notes="Organ: Head; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according

Bonafdo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with Ecor I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is CGAATCAAT. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH)."

ORIGIN

Query Match 60.7%; Score 593.8; DB 7; Length 710;

Best Local Similarity 92.8%; Pred. No. 5.1e-149;

Matches 655; Conservative 0; Mismatches 48; Indels 3; Gaps 3;

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Db 1 TGTAAATGGGGCGAGCTGTTTTCCATTTGTCGAGAGCGGGTGTCTCTGAGGACCG 60

Qy 336 CACACGTTTCTATGTTGCAGAAATTTGCTCTGCTTGGACTATCTACATTTCCGGAAGAT 395

Db 61 CACACGTTTCTATGTTGCAGAAATTTGCTCTGCTTGGACTATCTACATTTCCGGAAGAT 120

Qy 396 TGTGTACCGTGATCTCAAGTTGGAGAAATTTGATGCTAGATAAGGATGGCCATATAAAAT 455

Db 121 TGTGTACCGTGATCTCAAGTTGGAGAAATTTGATGCTAGATAAGGATGGCCATATAAAAT 180

Qy 456 TACAGATTTTGGACTTTGCAAGAAGGGATCACAGATGCAAGCCACCATGAAGACATTTCTG 515

Db 181 TACGATTTTGGGCTTTGCAAGAAGGGATCACAGATGCAAGCCACCATGAAGACATTTCTG 240

Qy 516 TGGCACTTCCAGAAATATCTGGCACCAGAGGTGTTAGAGATAAATGACTATATGCGCAGCAGT 575

Db 241 TGGCACCACAGAGTACTTGGCACCAGAGGTATTAGAAGATAAATGACTATATGCGCAGCAGT 300

Qy 576 AGACTGTGGGGCTTAGGGTTGTGTATGATAAATGATGTGGGAGGTTACCTTTCTA 635

Db 301 GGACTGTGGGGCTTAGGGTTGTGTATGATAAATGATGTGGGAGGTTACCTTTCTA 360

Qy 636 CAACGAGGACCATGAGAAATCTTTTGAATTAATTAATGAAGACATTAATTTCTCTCG 695

Db 361 CAACGAGGACCATGAGAAATCTTTTGAATTAATTAATGAAGACATTAATTTCTCTCG 420

Qy 696 AACACTCTTTCAGATGCAAAATCATTTGCTTTTTCAGGGCTCTTGTATAAGGATCCAAATAA 755

Db 421 AACACTCTTTCAGATGCAAAATCATTTGCTTTTTCAGGGCTCTTGTATAAGGATCCAAATAA 480

Qy 756 ACGCTTGGT-GGAGGACGAGATGATGCAAAAGAAATATGAGACAGATTTCTTCTC-T 813

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661 AACACCACCTGANAAGTATGACGACGCGCATGGCGCATGGAC 706
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Search completed: February 15, 2006, 06:28:03
Job time : 3884 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 05:23:16 ; Search time 4968 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	978	100.0	1436	6	AX026530 Sequence
3	978	100.0	1440	6	BD142211 Method fo
4	978	100.0	1440	11	AY335691 Synthetic
5	978	100.0	1440	11	AY893474 Synthetic
6	978	100.0	1440	11	AY893919 Synthetic
7	978	100.0	1445	8	BC020479 Homo sapi
8	978	100.0	1547	6	BD251226 Human Akt
9	978	100.0	1547	6	AR593589 Sequence
10	978	100.0	1547	6	AX026529 Sequence
11	978	100.0	1547	8	AJ245709 Homo sapi
12	978	100.0	1651	6	CQ714620 Sequence
13	978	100.0	1706	8	AF085234 Homo sapi
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26	584.8	59.8	1808	5	AF317656 Xenopus l
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30	527	53.9	1741	9	U22445 Mus musculu
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SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	1 (bases 1 to 1436)						
AUTHORS	Measure,S.L.J. and Richardson,A.						
TITLE	Human Akt-3						
JOURNAL	Patent: JP 2002535964-A 2 29-OCT-2002;						
COMMENT	JANSEN PHARMACEUTICA NV						
	OS Homo sapiens (human)						
	PN JP 2002535964-A/2						
	PD 29-OCT-2002						
	PF 17-DEC-1999 JP 2000589669						
	PR 22-DEC-1998 GB 9828375.7						
	PI STEFAN LEO JOZEF WASURE,ALAN RICHARDSON						
	PC C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K39/395,A61K48/00, PC						
	A61P35/00,						
	PC A61P43/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/						
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RESULT 2
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DEFINITION Sequence 2 from Patent WO0037613.
ACCESSION AX026530
VERSION AX026530.1 GI:10187718
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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            Homnidae; Homo.
REFERENCE 1
AUTHORS Masure,S.L. and Richardson,A.
TITLE Human akt-3
JOURNAL Patent: WO 0037613-A 2 29-JUN-2000;
          MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN
          PHARMACEUTICA NV (BE)
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Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTCAACCCCATATAAAGAAAGACAATGAATGATTTTGACCTATTGAACTACTAGGT 60
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Qy 61 AAAGGCACTTTGGGAAAAGTATTTTGGTTCGAGAGAAGGCAAGTGAAATACTATGCT 120
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AUTHORS	Tsuruo T., Fujita N. and Sato S.		
TITLE	Method for controlling apoptosis and polypeptide controlling		
JOURNAL	Patent: WO 0215925-A 5 28-FEB-2002;		
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	PC	A61K38/17, A61K38/45, A61K39/395, A61K45/00, A61P43/00, A61P3/08, A61P35/00,	
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Best Local Similarity		100.0%;	Pred. No. 4.1e-206;
Matches	978;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	TCTACAACCCATCAATAAGAAAGACAAATGATGATTTTGACTATTGTAATTTGAACTACTAGCT	60
Db	406	TCTACAACCCATCAATAAGAAAGACAAATGATGATTTTGACTATTGTAATTTGAACTACTAGCT	465

QY	61	AAAGGCACTTTTGGGAAAGTTATTTTGGTTGCGAGAGAGGCAAGTGGAAAAATACATATGCT	120
Db	466	AAAGGCACTTTTGGGAAAGTTATTTTGGTTGCGAGAGAGGCAAGTGGAAAAATACATATGCT	525
QY	121	ATGAGAGATCTTGAAGAAAGAGTCAATTATGCAAAAGGATGAAGTGGCAGACACTCTAACT	180
Db	526	ATGAGAGATCTTGAAGAAAGAGTCAATTATGCAAAAGGATGAAGTGGCAGACACTCTAACT	585
QY	181	GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCCTTGAATAATTTCCCTTC	240
Db	586	GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCCTTGAATAATTTCCCTTC	645
QY	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTC	300
Db	646	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTC	705
QY	301	CATTTGTCGAGAGAGCGGTTCTCTGAGAGACCGCACACAGTTTCTATGGTCAGAAAT	360
Db	706	CATTTGTCGAGAGAGCGGTTCTCTGAGAGACCGCACACAGTTTCTATGGTCAGAAAT	765
QY	361	GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	420
Db	766	GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	825
QY	421	AATCTAATGCTGGCAAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTGCAAGNA	480
Db	826	AATCTAATGCTGGCAAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTGCAAGNA	885
QY	481	GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGCACCTCCAGAAATATCTGCACCA	540
Db	886	GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGGCCTCCAGAAATATCTGCACCA	945
QY	541	GAGGTGTTAGAAGATAATGACTATGCGCGAGCAGTAGACTGGTGGGGCTTAGGGTTGTC	600
Db	946	GAGGTGTTAGAAGATAATGACTATGCGCGAGCAGTAGACTGGTGGGGCTTAGGGTTGTC	1005
QY	601	ATGTAATAAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATGAGAACTTTT	660
Db	1006	ATGTAATAAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATGAGAACTTTT	1065
QY	661	GAATTAATAATTAATGGAAGACATTTAAATTTCTCCTCGAAACACTCTCTTCAGATGCAAAATCA	720
Db	1066	GAATTAATAATTAATGGAAGACATTTAAATTTCTCCTCGAAACACTCTCTTCAGATGCAAAATCA	1125
QY	721	TTGCTTTTCAGGCTCTTGATTAAGATCCAAATAAAGCGCTTGGTGGAGGCCAGATGAT	780
Db	1126	TTGCTTTTCAGGCTCTTGATTAAGATCCAAATAAAGCGCTTGGTGGAGGCCAGATGAT	1185
QY	781	GCAAAAGAAATTAATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	840
Db	1186	GCAAAAGAAATTAATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	1245
QY	841	AAAAAGCTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATATATATTTT	900
Db	1246	AAAAAGCTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATATATATTTT	1305
QY	901	GATGAAGAAATTAACAGCTCAGACTTATCAATAACACACCTGAAATAATATGATGAGGAT	960
Db	1306	GATGAAGAAATTAACAGCTCAGACTTATCAATAACACACCTGAAATAATATGATGAGGAT	1365
QY	961	GGTATGGACTGCATGGAC	978
Db	1366	GGTATGGACTGCATGGAC	1383
RESULT 4			
AY335691			
LOCUS	AY335691	1440 bp	mRNA linear SYN 08-JUN-2005
DEFINITION	Synthetic construct Homo sapiens v-akt murine thymoma viral		
ACCESSION	AY335691		
VERSION	AY335691.1	GI:33304020	

KEYWORDS	FLI_CDNA.
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	1 (bases 1 to 1440)
AUTHORS	Park,J., Hu,Y., Murthy,T.V.S., Vannberg,F., Shen,B., Rolfs,A., Hutti,J.E., Canclley,L.C., LaBaer,J., Harlow,E. and Brizuela,L.
TITLE	Building a human kinase gene repository: Bioinformatics, molecular cloning, and functional validation
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)
PUBMED	15928075
REFERENCE	2 (bases 1 to 1440)
AUTHORS	Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D., Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E., LaBaer,J. and Brizuela,L.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA
COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
FEATURES	Location/Qualifiers
source	1..1440
	/organism="synthetic construct"
	/mol_type="mRNA"
	/db_xref="taxon:32630"
	/clones="FLH00146.01L"
	/tissue_type="placenta and brain"
	/clone_libs="First strand cDNA from placenta and brain"
	/lab_hosts="DH5alpha T1 resistant"
	/note="vector: pDNR-Dual"
gene	1..>1440
CDS	/gene="AKT3"
	1..>1440
	/gene="AKT3"
	/note="protein kinase B, gamma; Mutations: Stop->Leu"
	/codon_start=1
	/transl_table=11
	/product="v-akt murine thymoma viral oncogene-like 3"
	/protein_id="AAQ02518.1"
	/db_xref="GI:3304021"
	/translation="MSDVTIVKGVQKRGYIKNRPYLLKTDGSGFIYKKEKPOD VLPYPLNFSVAKCOLMTERPKPNTFIIRCLQWTVIERTPHVDTPPEEREWTEAI QAVADRLQROSEERWNCSPPTSDI NIGEEEMDASTHKKRMNDPDLKLGKTRG KVILVREKASKYAMKILKEVLIADKVAHTLTSRVLKNTPHPLTSLKYSFPQK LRLCFVMEYVNGGSLFFHLRSRVSFSDTRFYGAIEVSALDYHSGKI VTRDLKEN VMYEMGCRLPFPYVQNDKEGLFELIMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGG PDDAKEIMRHSFFSGVNVQVDYDKLVPPFPKQVTSOTDTRYPDEEFTATTITPPE KYDEGDMDCMDNRRPFPQFSYASGREL"
ORIGIN	
Query Match	100.0%; Score 978; DB 11; Length 1440;
Best Local Similarity	100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 TCTCAACCCATCAATAAGAAAGACATGATGATCTTTTGACTATTTCGAACACTACTAGGT 60
Db	406 TCTCAACCCATCAATAAGAAAGACATGATGATCTTTTGACTATTTCGAACACTACTAGGT 465
Qy	61 AAAGGCATTTTGGGAAAGTTATTTTTGGTTCGAGAGAAGGCAAGTGGAAATACTATGCT 120
Db	466 AAAGGCATTTTGGGAAAGTTATTTTTGGTTCGAGAGAAGGCAAGTGGAAATACTATGCT 525
Qy	121 ATGAAGATCTGAAGAAAGATGATCTATTTCGAAAGGATGAAGTGGCACACACTCTTAAC 180

Db	526 ATGAAGATCTGAAGAAAGATGATCTATTTCGAAAGGATGAAGTGGCACACACTCTTAAC 585
Qy	181 GAAAGCAGAGTGATTAAAGAAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240
Db	586 GAAAGCAGAGTGATTAAAGAAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 645
Qy	241 CAGACAAAACACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 300
Db	646 CAGACAAAACACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 705
Qy	301 CATTGTGCGAGAGACGGGTGTTCTCTGAGGACCGGCACACAGTTTCTATGTCGAGAAATT 360
Db	706 CATTGTGCGAGAGACGGGTGTTCTCTGAGGACCGGCACACAGTTTCTATGTCGAGAAATT 765
Qy	361 GTCTCTCCCTTGGACTACTTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db	766 GTCTCTCCCTTGGACTACTTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 825
Qy	421 AATCTAATGCTGGACAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTTGCAGAA 480
Db	826 AATCTAATGCTGGACAAAGATGGCCACATATAAAATTTACAGATTTTGGACTTTTGCAGAA 885
Qy	481 GGGATCACAGATGCAGCACCACATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACC 540
Db	886 GGGATCACAGATGCAGCACCACATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACC 945
Qy	541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTC 600
Db	946 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTC 1005
Qy	601 ATGTATGAAATGATGTGGGAGGTTACCTTTTCTACAAACGAGGACCATGAGAAACTTTTT 660
Db	1006 ATGTATGAAATGATGTGGGAGGTTACCTTTTCTACAAACGAGGACCATGAGAAACTTTTT 1065
Qy	661 GAATTAATATTAATGGAAGACATTAATTTCTTCGAAACACTCTCTTCAGATGCAAAATCA 720
Db	1066 GAATTAATATTAATGGAAGACATTAATTTCTTCGAAACACTCTCTTCAGATGCAAAATCA 1125
Qy	721 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGAGGACCAAGATGAT 780
Db	1126 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGAGGACCAAGATGAT 1185
Qy	781 GCAAAAGAAATATGAGACACAGTTTCTTCTGTGAGTAAACTGGCAAGATGTATATGAT 840
Db	1186 GCAAAAGAAATATGAGACACAGTTTCTTCTGTGAGTAAACTGGCAAGATGTATATGAT 1245
Qy	841 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 900
Db	1246 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 1305
Qy	901 GATGAAGAAATTTACAGCTCAGACTATTACAAATACACCACTGAAAAATATGATGAGAT 960
Db	1306 GATGAAGAAATTTACAGCTCAGACTATTACAAATACACCACTGAAAAATATGATGAGAT 1365
Qy	961 GGTATGACCTGCATGGAC 978
Db	1366 GGTATGACCTGCATGGAC 1383
RESULT 5	
AY893474	
LOCUS	AY893474 1440 bp mRNA linear SYN 16-MAR-2005
DEFINITION	Synthetic construct Homo sapiens clone FLH127839.01X v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, complete cds.
ACCESSION	AY893474
VERSION	AY893474.1 GI:60819745
KEYWORDS	Human ORF Project.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	1 (bases 1 to 1440)
AUTHORS	Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.

TITLE
Cloning of human full-length CDS FLEXGene in Gateway(TM) recombinational vector system

JOURNAL
Unpublished

AUTHORS
2 (bases 1 to 1440)
Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.

TITLE
Direct Submission

JOURNAL
Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA

COMMENT
This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned with normalized stop-codon. AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.

FEATURES
Location/Qualifiers
1..1440
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="FLH127839.01X"
/lab_host="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library from placenta and brain"
1..1440
/gene="AKT3"
1..1440
/gene="AKT3"
/note="protein kinase B gamma"
/codon_start=1
/transl_table=11
/product="v-akt murine thymoma viral oncogene-like 3"
/protein_id="AAK34511.1"
/db_xref="GI:60819746"
/translation="MSDVTIVKGEVQKRGVYKINRPRYFLKTKDGSFYGKPKQD VDLPLNFSVQKLMKTPKNTFIIRCLQWTVIERFTFHDVTPPEEREWEPEAI QAVDLROREBERMNCPSOINDIGBEEMDASTTHKRTKMDNPDYLLKLGKTFG KVLVREKASGYAMKLLKEVIAKDEVAHTLTSVRLKNTKRPFLTSLKYSQTK DRLCFMVEYNGELFFHLRSRVSERTRFYGAELVSDYLHSGIKVTRDLKLEN LMLDKDHIKITDFGLCKEGITDAKMTFCGTPYLAPEVLNDNDYGRAVDWNLGV VNYEMWCGRLPPYNDHKLFIELIMDEIKFPTLSDAKSLGLLIKDNKRLGGG PDDAKEINRHSFSGVNWVDVKKLVPPFKPQVTSQTDTRYFDEBFTAQITITPPE KYDEGDMDCMDNERRPHFPQPSYSASGRE"

gene
1..1440

CDS
1..1440

ORIGIN

Query Match 100.0%; Score 978; DB 11; Length 1440;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTACACCCATCAATAAGAAAGACAATGAATGATTTTGACTATTGAACTACTAGGT 60
DB 406 TCTACACCCATCAATAAGAAAGACAATGAATGATTTTGACTATTGAACTACTAGGT 465
QY 61 AAAGGCACATTTGGGAAAGTATTTTGGTTTCAGAGAAGCGCAAGTGGAAATCTATGCT 120
DB 466 AAAGGCACATTTGGGAAAGTATTTTGGTTTCAGAGAAGCGCAAGTGGAAATCTATGCT 525
QY 121 ATGAAGATCTCAAGAAAGAAAGTCATATTATTCAGAAAGGATGAAGTGGCACACCTCTAACT 180
DB 526 ATGAAGATCTCAAGAAAGAAAGTCATATTGCAAGAGATGAAGTGGCACACCTCTAACT 585
QY 181 GAAGCAGAGTATTAAGACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC 240
DB 586 GAAGCAGAGTATTAAGACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC 645
QY 241 CAGACAAAAGACCGTTTGTGTTTGGTGGTGAATATGTTAAATGGGGCGAGCTGTTTTC 300
DB 646 CAGACAAAAGACCGTTTGTGTTTGGTGGTGAATATGTTAAATGGGGCGAGCTGTTTTC 705

QY 301 CATTTGTCGAGAGAGCGGGTCTTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT 360
DB 706 CATTTGTCGAGAGAGCGGGTCTTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT 765
QY 361 GTCTCTGCTTGGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
DB 766 GTCTCTGCTTGGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 825
QY 421 AATCTAATGCTGGCAAAAGATGGCCACATAAAAAATTACAGATTTTGGACTTTGCAAAAGAA 480
DB 826 AATCTAATGCTGGCAAAAGATGGCCACATAAAAAATTACAGATTTTGGACTTTGCAAAAGAA 885
QY 481 GGGATCAGAGATGCGAGCCACCATGAGACATCTCTGGCACTCCAGAAATATCTGCGACCA 540
DB 886 GGGATCAGAGATGCGAGCCACCATGAGACATCTCTGGCACTCCAGAAATATCTGCGACCA 945
QY 541 GAGGTGTTAGAAAGATAATGACTATATGGCGAGCAGTAGACTGTGTGGGGCTAGGGGTTGTC 600
DB 946 GAGGTGTTAGAAAGATAATGACTATATGGCGAGCAGTAGACTGTGTGGGGCTAGGGGTTGTC 1005
QY 601 ATGTATGAAATGATGTGTGGGAGGTTTACCTTTCTACAACCGAGGACCATGAGAAACTTTTT 660
DB 1006 ATGTATGAAATGATGTGTGGGAGGTTTACCTTTCTACAACCGAGGACCATGAGAAACTTTTT 1065
QY 661 GAAATTAATTAATGGAAGACATTAATAATTTCTCGAACAATCTCTTCAGATGCAAAATCA 720
DB 1066 GAAATTAATTAATGGAAGACATTAATAATTTCTCGAACAATCTCTTCAGATGCAAAATCA 1125
QY 721 TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAACGCTTGTGTGGAGGACCATGATGAT 780
DB 1126 TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAACGCTTGTGTGGAGGACCATGATGAT 1185
QY 781 GCAAAAGAAATTAATGAGACACAGATTTTCTCTGAGGTAAACTGGCAAGATGTATATGAT 840
DB 1186 GCAAAAGAAATTAATGAGACACAGATTTTCTCTGAGGTAAACTGGCAAGATGTATATGAT 1245
QY 841 AAAAGAGCTTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 900
DB 1246 AAAAGAGCTTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 1305
QY 901 GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACCACCTGAAATAATATGATGAGAT 960
DB 1306 GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACCACCTGAAATAATATGATGAGAT 1365
QY 961 GGTATGAGCTGATGATGAG 978
DB 1366 GGTATGAGCTGATGAG 1383

RESULT 6
AY893919
LOCUS AY893919
DEFINITION Synthetic construct Homo sapiens clone FLH127915.01L v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, partial cds.
ACCESSION AY893919
VERSION AY893919.1 GI:60831074
KEYWORDS synthetic construct
SOURCE Human ORF Project.
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1440)
AUTHORS Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
TITLE Cloning of human full-length CDS FLEXGene in Gateway(TM) recombinational vector system
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1440)
AUTHORS Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
TITLE Direct Submission
JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA

COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequence). Each clone is clonally isolated and full-length sequence-verified.

FEATURES
Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/cnames="FLH127915_01L"
/lab_hosts="Escherichia coli DH5alpha T1 resistant"
/note="derived from Homo sapiens first strand cDNA library from placenta and brain"
1..>1440
/gene="AKT3"
1..>1440
/gene="AKT3"
/note="protein kinase B gamma"
/codon_start=1
/transl_table=1
/product="v-akt murine thymoma viral oncogene-like 3"
/protein_id="AA336956.1"
/db_xref="GI:60831075"
/translation="MSDVTVIKGVQKRGVEIKWPRVFLKTKDGSFIGYKEKPPD
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KYDEGDMDCMDNERRPHFPQFSASGREL"

ORIGIN

Query Match 100.0%; Score 978; DB 11; Length 1440;
Best Local Similarity 100.0%; Pred. No. 4.1e-206; Mismatches 0; Indels 0; Gaps 0;
Matches 978; Conservative 0;
Qy 1 TCTACAACCCATCAATAAGAAAGACATGAATGATTGACTATTGAACTACTAGGT 60
Db 406 TCTACAACCCATCAATAAGAAAGACATGAATGATTGACTATTGAACTACTAGGT 465
Qy 61 AAAGGCACTTTGGGAAAGTATTATTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120
Db 466 AAAGGCACTTTGGGAAAGTATTATTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 525
Qy 121 ATGAAGATCTTGAAGAGAGTCAATATTGCAAGAGTGAAGTGGCACACACTCTAACT 180
Db 526 ATGAAGATCTTGAAGAGAGTCAATATTGCAAGAGTGAAGTGGCACACACTCTAACT 585
Qy 181 GAAAGCAGAGTATTAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATCTCTTC 240
Db 586 GAAAGCAGAGTATTAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATCTCTTC 645
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC 300
Db 646 CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC 705
Qy 301 CATTTGTCGAGAGCGGGTCTCTCTGAGACCGCACACGCTTTCTATGGTGCGAATTT 360
Db 706 CATTTGTCGAGAGCGGGTCTCTCTGAGACCGCACACGCTTTCTATGGTGCGAATTT 765
Qy 361 GTCTCTGCTTTGGACTATCTACATTCCGGAAGAGTTGTGACCGTGATCTCAAGTTGGAG 420
Db 766 GTCTCTGCTTTGGACTATCTACATTCCGGAAGAGTTGTGACCGTGATCTCAAGTTGGAG 825
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGACTTTGCAAGAA 480

Db 826 AATCTAATGCTGGACAAAGATGGCCACATAAAAATTTACAGATTTTGGACTTTGCAAGAA 885
Qy 481 GGGATCACAGATCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 886 GGGATCACAGATCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 945
Qy 541 GAGGTGTTAGGAAGATTAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTTAGGGTTGTC 600
Db 946 GAGGTGTTAGGAAGATTAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTTAGGGTTGTC 1005
Qy 601 ATGTATGAATATGATGTGGGAGTTTACCTTTCTACACAGGACCATGAGAAATCTTTT 660
Db 1006 ATGTATGAATATGATGTGGGAGTTTACCTTTCTACACAGGACCATGAGAAATCTTTT 1065
Qy 661 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db 1066 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1125
Qy 721 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGAGGACCAAGATGAT 780
Db 1126 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGAGGACCAAGATGAT 1185
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCGGAGTAACTGGCAAGATGTATATGAT 840
Db 1186 GCAAAAGAAATATGAGACACAGTTTCTCTCGGAGTAACTGGCAAGATGTATATGAT 1245
Qy 841 AAAAAGCTTCTGCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTT 900
Db 1246 AAAAAGCTTCTGCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTT 1305
Qy 901 GATGAAGAATTTACAGCTCAGCTATTATTAACATTAACACCACTGAAAAATATGATGAGAT 960
Db 1306 GATGAAGAATTTACAGCTCAGCTATTATTAACATTAACACCACTGAAAAATATGATGAGAT 1365
Qy 961 GGTATGACGTCGATGGAC 978
Db 1366 GGTATGACGTCGATGGAC 1383

RESULT 7
BC020479 1445 bp mRNA linear PRI 28-JUL-2005
LOCUS Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein
DEFINITION kinase B, gamma), mRNA (cDNA clone IMAGE:3867931), partial cds.
BC020479
ACCESSION BC020479.1 GI:18042842
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1445)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schectz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalek, U., Smaluk, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
TITLE

Hominidae; Homo.
1 (bases 1 to 1547)
Masure,S.L.J. and Richardson,A.
Human Akt-3
Patent: JP 2002535964-A 1 29-OCT-2002;
JANSSEN PHARMACEUTICA NV
OS Homo sapiens (human)
PN JP 2002535964-A/1
PD 29-OCT-2002
PF 17-DEC-1999 JP 2000589669
PR 22-DEC-1998 GB 9828375.7
PI STEFAN LEO JOZEF MASURE,ALAN RICHARDSON
PC C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K39/395,A61K48/00,PC
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PC A61P43/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
PC 12,C12Q1/02,
PC C12Q1/48,G01N33/15,G01N33/50,G01N33/53,G01N33/566//C12P21/08,
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ORIGIN
Query Match 100.0%; Score 978; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR593589 1547 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 1 from patent US 6809194.
ACCESSION AR593589
VERSION AR593589.1 GI:56642796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1547)
AUTHORS Reinhard,C. and Jefferson,A.B.
TITLE Akt3 inhibitors
JOURNAL Patent: US 6809194-A 1 26-OCT-2004;
Chiron Corporation; Emeryville, CA
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Query Match 100.0%; Score 978; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AX026529
LOCUS AX026529 1547 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 1 from Patent W00037613.
ACCESSION AX026529
VERSION AX026529.1 GI:10187717
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominae; Homo.

REFERENCE 1
AUTHORS Masure,S.L. and Richardson,A.
TITLE Human akt-3
JOURNAL Patent: WO 0037613-A 1 29-JUN-2000;
MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN
PHARMACEUTICA NV (BE)

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Query Match 100.0%; Score 978; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 4.1e-206; Mismatches 0; Indels 0; Gaps 0;
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AF124141.1 GI:4757578
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Hominidae; Homo.
REFERENCE
1 (bases 1 to 1708)
Brodbeck,D., Cron,P. and Hemmings,B.A.
A human protein kinase Bgamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain
J. Biol. Chem. 274 (14), 9133-9136 (1999)
PUBMED 10092583
REFERENCE
2 (bases 1 to 1708)
Brodbeck,D., Cron,P. and Hemmings,B.A.
Direct Submission
Submitted (27-JAN-1999) Friedrich Miescher-Institut,
Maulbeerstrasse 66, Basel 4058, Switzerland
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Location/Qualifiers
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Query Match 100.0%; Score 978; DB 8; Length 1708;
Best Local Similarity 100.0%; Pred. No. 4e-206;
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DB 946 GAGGTGTTAGAGATTAATCACTATGCGCCGACAGTAGACTGTGGGGCCCTAGGGGTTGTC 1005
QY 601 ATGTATGAATGATGTGGGAGGTGTACCTTTCTACAACAGGACCATGAGAAATCTTTT 660
DB 1006 ATGTATGAATGATGTGGGAGGTGTACCTTTCTACAACAGGACCATGAGAAATCTTTT 1065
QY 661 GAATTAATATTAATGGAAGACATTAATTTCTCTGGAACACTCTCTTCAGATGCAAAATCA 720
DB 1066 GAATTAATATTAATGGAAGACATTAATTTCTCTGGAACACTCTCTTCAGATGCAAAATCA 1125
QY 721 TTGCTTTTCAGGCTCTTGATTAAGGATCCAAATTAACGCTTTGGTGGAGGACCATGAT 780
DB 1126 TTGCTTTTCAGGCTCTTGATTAAGGATCCAAATTAACGCTTTGGTGGAGGACCATGAT 1185
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DB 1306 GATGAAGAATTTTACAGCTCAGACTATTACAATAACACCACTGAAATAATATGATGAGAT 1365
QY 961 GGTATGGACTGCATGGAC 978
DB 1366 GGTATGGACTGCATGGAC 1383
RESULT 2
AX026530 1436 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 2 from Patent WO0037613.
ACCESSION AX026530
VERSION AX026530.1 GI:10187718
KEYWORDS
SOURCE
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homidae; Homo.
REFERENCE
    Masure, S.L. and Richardson, A.
    AUTHORS Human akt-3
    TITLE Patent: WO 0037613-A 2 29-JUN-2000;
    JOURNAL MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN
    PHARMACEUTICA NV (BE)
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 466 AAAGGCACCTTTGGGAAAGTTATTTTGGTTTCGAGAGAAGGCAAGTGGAAATACATGCT 525
QY 121 ATGAAGATTTCTGAAGAAGAAGTCAATTTTGGTTTCGAGAGAAGGCAAGTGGCAACACTCTAACT 180
DB 526 ATGAAGATTTCTGAAGAAGAAGTCAATTTTGGTTTCGAGAGAAGGCAAGTGGCAACACTCTAACT 585
QY 181 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATTTCCCTTC 240
DB 586 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATTTCCCTTC 645
QY 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300
DB 646 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 705
QY 301 CATTTGTGAGAGAGCGGTGTTCTCTGAGGACCGGACACAGTTTCTATGGTGCAGAAAT 360
DB 706 CATTTGTGAGAGAGCGGTGTTCTCTGAGGACCGGACACAGTTTCTATGGTGCAGAAAT 765
QY 361 GTCTCTGCTCGACTATCTACATTCGGAAGAGTTGTACCGTGATCTCAAGTTGGAG 420
DB 766 GTCTCTGCTCGACTATCTACATTCGGAAGAGTTGTACCGTGATCTCAAGTTGGAG 825
QY 421 AATCTAATGCTGGAACAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480
DB 826 AATCTAATGCTGGAACAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 885
QY 481 GGGATCAGAGATGCAAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGACA 540
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QY 541 GAGGTGTTAGAGATTAATCACTATGCGCCGACAGTAGACTGTGGGGCCCTAGGGGTTGTC 600
DB 946 GAGGTGTTAGAGATTAATCACTATGCGCCGACAGTAGACTGTGGGGCCCTAGGGGTTGTC 1005
QY 601 ATGTATGAATGATGTGGGAGGTGTACCTTTCTACAACAGGACCATGAGAAATCTTTT 660
DB 1006 ATGTATGAATGATGTGGGAGGTGTACCTTTCTACAACAGGACCATGAGAAATCTTTT 1065
QY 661 GAATTAATATTAATGGAAGACATTAATTTCTCTGGAACACTCTCTTCAGATGCAAAATCA 720
DB 1066 GAATTAATATTAATGGAAGACATTAATTTCTCTGGAACACTCTCTTCAGATGCAAAATCA 1125
QY 721 TTGCTTTTCAGGCTCTTGATTAAGGATCCAAATTAACGCTTTGGTGGAGGACCATGAT 780
DB 1126 TTGCTTTTCAGGCTCTTGATTAAGGATCCAAATTAACGCTTTGGTGGAGGACCATGAT 1185
QY 781 GCAAAAGAAATATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840
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Qy	481	GGGATCACAGATGCAGCCACCACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGCACCA	540
Db	886	GGGATCACAGATGCAGCCACCACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGCACCA	945
Qy	541	GAGGTGTTAGAAATAATGACTATGGCCGAGAGTAGACTGGTGGGGCTTAGGGTTGTC	600
Db	946	GAGGTGTTAGAAATAATGACTATGGCCGAGAGTAGACTGGTGGGGCTTAGGGTTGTC	1005
Qy	601	ATGTATGAAATGATCTGTGGGAGGTTACCTTTCTACACACAGGACCATGAGAACTTTT	660
Db	1006	ATGTATGAAATGATCTGTGGGAGGTTACCTTTCTACACACAGGACCATGAGAACTTTT	1065
Qy	661	GAATTAATATTAATGGAAGACATTAATAATTCCTCGAACACTCTCTTCAGATGCCAAATCA	720
Db	1066	GAATTAATATTAATGGAAGACATTAATAATTCCTCGAACACTCTCTTCAGATGCCAAATCA	1125
Qy	721	TTGCTTTTCAGGGCTCTTGATTAAGGATCCAAATTAACCCCTTGGTGGAGGACCAAGATGAT	780
Db	1126	TTGCTTTTCAGGGCTCTTGATTAAGGATCCAAATTAACCCCTTGGTGGAGGACCAAGATGAT	1185
Qy	781	GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAAACTGCGAAGATGTATATGAT	840
Db	1186	GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAAACTGCGAAGATGTATATGAT	1245
Qy	841	AAAAAGCTTGACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT	900
Db	1246	AAAAAGCTTGACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT	1305
Qy	901	GATGAAGAAATTTACAGCTCAGACATTTTACAAATTAACCCACTGAAAATATGATGAGAT	960
Db	1306	GATGAAGAAATTTACAGCTCAGACATTTTACAAATTAACCCACTGAAAATATGATGAGAT	1365
Qy	961	GGTATGGAATGCAATGGAC	978
Db	1366	GGTATGGAATGCAATGGAC	1383
RESULT 3			
BD142211		1440 bp	DNA linear PAT 18-SEP-2002
LOCUS	BD142211		
DEFINITION	Method for controlling apoptosis and polypeptide controlling		
ACCESSION	BD142211		
VERSION	BD142211.1	GI:23237156	
KEYWORDS	WO 0215925-A/5.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1440)		
TITLE	Tsuruo, T., Fujita, N. and Sato, S.		
JOURNAL	Method for controlling apoptosis and polypeptide controlling		
COMMENT	PATENT: WO 0215925-A 5 28-FEB-2002; KYOWA HAKKO KOGYO CO LTD, TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO OS Homo sapiens (human) PN WO 0215925-A/5 PD 28-FEB-2002 PF 22-AUG-2001 WO 2001JP007179 PR 22-AUG-2000 JP 00P 251529 PI TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO PC A61K38/17, A61K38/45, A61K39/395, A61K45/00, A61P43/00, A61P3/08, A61P35/00, PC A61P43/00, C07K14/47, C07K16/18, C12N1/15, C12N1/19 PC , C12N1/21, C12N5/10, PC C12P21/02, C12N15/09, G01N33/50, G01N33/15, G01N33/566, G01N33/68 CC human Akt3 FH Key FT source 1. .1440 FT Location/Qualifiers FT Location/Qualifiers 1. .1440		
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Db	406	TCACACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTGACATTTTGAACACTACTAGT	465
Qy	61	AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAAAGCAAGTCAAGTGGAAATATCTATGCT	120
Db	466	AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAAAGCAAGTGGAAATATCTATGCT	525
Qy	121	ATGAAGATTCTGAAGAAAGAGTCATTTATTTGCAAAAGATGAAGTGGCACACACTCTAACT	180
Db	526	ATGAAGATTCTGAAGAAAGAGTCATTTATTTGCAAAAGATGAAGTGGCACACACTCTAACT	585
Qy	181	GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTTCCCTTC	240
Db	586	GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTTCCCTTC	645
Qy	241	CAGACAAAAGACCGTTTGTGTGTTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC	300
Db	646	CAGACAAAAGACCGTTTGTGTGTTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC	705
Qy	301	CATTGTGCGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAAAATTT	360
Db	706	CATTGTGCGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAAAATTT	765
Qy	361	GTCTCTGCCCTTGGACTATCTACATTCGGGAAAGATCTGTACCGTGATCTCAAGTTGCGAG	420
Db	766	GTCTCTGCCCTTGGACTATCTACATTCGGGAAAGATCTGTACCGTGATCTCAAGTTGCGAG	825
Qy	421	AATCTAATGCTGGACAAAGATGGCCACATAAAAATTAACAGATTTTGACATTTTGCAAGAA	480
Db	826	AATCTAATGCTGGACAAAGATGGCCACATAAAAATTAACAGATTTTGACATTTTGCAAGAA	885
Qy	481	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	540
Db	886	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	945
Qy	541	GAGGTGTTAGAAATAATGACTATGGCCGAGAGTAGACTGGTGGGGCTTAGGGTTGTC	600
Db	946	GAGGTGTTAGAAATAATGACTATGGCCGAGAGTAGACTGGTGGGGCTTAGGGTTGTC	1005
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Db	1006	ATGTATGAAATGATGTTGGGAGGTTACCTTTCTACAAACGAGGACCATGAGAAACTTTTTT	1065
Qy	661	GAATTAATATTAATGGAAGACATTAATAATTCCTCGAACACTCTCTTCAGATGCCAAATCA	720
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Qy	721	TTGCTTTTCAGGGCTCTTGATTAAGGATCCAAATTAACCCCTTGGTGGAGGACCAAGATGAT	780
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Qy	781	GCAAAAGAAATATGAGACACAGTTTCTCTTCGGAGTAAACTGCGAAGATGTATATGAT	840
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Qy	901	GATGAAGAAATTTACAGCTCAGACATTTTACAAATTAACCCACTGAAAATATGATGAGAT	960
Db	1306	GATGAAGAAATTTACAGCTCAGACATTTTACAAATTAACCCACTGAAAATATGATGAGAT	1365

Qy	961	GGTATGCACTGCATGGAC	978	Matches	978;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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RESULT 4													
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LOCUS													
DEFINITION													
Synthetic construct Homo sapiens v-akt murine thymoma viral													
oncogene-like 3 (AKT3) mRNA, partial cds.													
ACCESSION													
AY335691													
VERSION													
AY335691.1 GI:33304020													
KEYWORDS													
FLI_CDNA.													
SOURCE													
synthetic construct													
ORGANISM													
other sequences; artificial sequences.													
REFERENCE													
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Park,J., Hu,Y., Murthy,T.V.S., Vannberg,F., Shen,B., Rolfs,A.,													
Hutti,J.E., Cantley,L.C., LaBaer,J., Harlow,E. and Brizuela,L.													
Building a human kinase gene repository: Bioinformatics, molecular													
cloning, and functional validation													
Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)													
JOURNAL													
PUBMED													
15928075													
REFERENCE													
2 (bases 1 to 1440)													
Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D.,													
Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E.,													
LaBaer,J. and Brizuela,L.													
Direct Submission													
Submitted (02-JUN-2003) Biological Chemistry and Molecular													
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,													
Cambridge, MA 02141-2023, USA													
TITLE													
This CDS clone is a part of a collection of human full-length													
expression clones generated by Harvard Institute of Proteomics.													
Each CDS has been cloned without stop-codon (to allow fusion with													
C-terminal tag). The CDS has been directionally cloned using BD													
In-Fusion(TM) cloning system between the SalI and HindIII sites of													
the pDNR-Dual vector. Additional sequences in the clone: 'ACC'													
after SalI site and before 'ATG' to provide Kozak consensus													
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reading frame.													
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ORIGIN													
Query Match 100.0%; Score 978; DB 11; Length 1440;													
Best Local Similarity 100.0%; Pred. NO. 4.1e-206;													

Query Match 100.0%; Score 978; DB 11; Length 1440;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;

LOCUS	AY893474	1440 bp	mRNA	linear	SYN 16-MAR-2005			
DEFINITION	Synthetic construct Homo sapiens clone FLH127839.01X v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, complete cds.							
ACCESSION	AY893474							
VERSION	AY893474.1	GI:60819745						
KEYWORDS	Human ORF Project.							
SOURCE	synthetic construct							
ORGANISM	other sequences; artificial sequences.							
REFERENCE	1 (bases 1 to 1440)							
AUTHORS	Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.							
TITLE	Cloning of human full-length CDS FLEXGene in Gateway(TM)recombinational vector system							
JOURNAL	Unpublished							
REFERENCE	2 (bases 1 to 1440)							
AUTHORS	Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.							
TITLE	Direct SubMISSION							
JOURNAL	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA							
COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Insititute of Proteomics. This ORF clone has been cloned with normalized stop-codon. ActB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.							
FEATURES	Location/Qualifiers							
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ORIGIN								
Query Match	100.0%;	Score 978;	DB 11;	Length 1440;				
Best Local Similarity	100.0%;	Pred. No. 4.le-206;						
Matches	978;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
Qy	1	TCTACAAACCCATCAATAAAGAAAGACAAATGAATGATTGTGACTATTTGAACACTAGGT	60					
Db	406	TCTACAAACCCATCAATAAAGAAAGACAAATGAATGATTGTGACTATTTGAACACTAGGT	465					
Qy	61	AAAGGCACCTTTGGGAAGTATTATTTGGTTCCGAGAGAAGCAAGTGGAAAATACTATGCT	120					
Db	466	AAAGGCACCTTTGGGAAGTATTATTTGGTTCCGAGAGAAGCAAGTGGAAAATACTATGCT	525					

Qy	121	ATGAAGATTCTTGAAGAAAGAGTCAATTATTGCAAGGATGAAGTGGCACACACTCTAACT	180		
Db	526	ATGAAGATTCTTGAAGAAAGAGTCAATTATTGCAAGGATGAAGTGGCACACACTCTAACT	585		
Qy	181	GAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATATCTTC	240		
Db	586	GAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTGAATATATCTTC	645		
Qy	241	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC	300		
Db	646	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC	705		
Qy	301	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGCAAAATT	360		
Db	706	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGCAAAATT	765		
Qy	361	GTCTCTGCCCTTGGACATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	420		
Db	766	GTCTCTGCCCTTGGACATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	825		
Qy	421	AATCTAATGCTGGACAAAGATGGCCACATATAAATAATACAGATTTTGGACCTTTGCAAGAA	480		
Db	826	AATCTAATGCTGGACAAAGATGGCCACATATAAATAATACAGATTTTGGACCTTTGCAAGAA	885		
Qy	481	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	540		
Db	886	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	945		
Qy	541	GAGTGTTTGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTC	600		
Db	946	GAGTGTTTGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTC	1005		
Qy	601	ATGTATGAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATGAGAACTTTTT	660		
Db	1006	ATGTATGAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATGAGAACTTTTT	1065		
Qy	661	GAATTAATTAATTAATGAAGACATTTAAATTTCTCGCAACACTCTCTTCAGAGATGCAAAATCA	720		
Db	1066	GAATTAATTAATTAATGAAGACATTTAAATTTCTCGCAACACTCTCTTCAGAGATGCAAAATCA	1125		
Qy	721	TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGGAGCCAGATGAT	780		
Db	1126	TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGGAGCCAGATGAT	1185		
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Qy	841	AAAAAGCTTTGACTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTT	900		
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Db	1366	GGTATGACCTGCATGGAC	1383		
RESULT 6					
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LOCUS	AY893919				
DEFINITION	Synthetic construct Homo sapiens clone FLH127915.01L v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, partial cds.				
ACCESSION	AY893919				
VERSION	AY893919.1				
KEYWORDS	Human ORF Project.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 1440)				

AUTHORS	Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
TITLE	Cloning of human full-length CDS FLEXGene in Gateway(TM) recombinational vector system
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1440)
AUTHORS	Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
TITLE	Direct Submission
JOURNAL	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AtbB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequence). Each clone is clonally isolated and full-length sequence-verified.
FEATURES	Location/Qualifiers
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	/note="derived from Homo sapiens first strand cDNA library from placenta and brain"
gene	1..>1440
CDS	/gene="AKT3"
	1..>1440
	/gene="AKT3"
	/note="protein kinase B gamma"
	/codon_start=1
	/transl_table=11
	/product="v-akt murine thymoma viral oncogene-like 3"
	/protein_id="AAK36956.1"
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Query Match	100.0%; Score 978; DB 11; Length 1440;
Best Local Similarity	100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACATATTGTAAGAACTACTAGT 60
DB	
QY	406 TCTACAACCCATCATAAAAGAAAGACAATGAATGATTTTGACATATTGTAAGAACTACTAGT 465
DB	
QY	61 AAAGGCACATTTGGGAAGCTATTTTGGTTCGAGAGCAAGCAAGTGGAAATACTATGCT 120
DB	
QY	466 AAAGGCACATTTGGGAAGCTATTTTGGTTCGAGAGCAAGCAAGTGGAAATACTATGCT 525
DB	
QY	121 ATGAAGATTCTGAAGAAGAAAGTCATATTATGCAAGGATGAAGTGGCCACACACTCTAACT 180
DB	
QY	526 ATGAAGATTCTGAAGAAGAAAGTCATATTATGCAAGGATGAAGTGGCCACACACTCTAACT 585
DB	
QY	181 GAAAGCAGAGTATTAAGAACAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC 240
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QY	586 GAAAGCAGAGTATTAAGAACAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC 645
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QY	241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTC 300
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Db	646 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTC 705
QY	301 CATTTTGTGAGAGAGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGTTGAGAAAT 360
DB	
QY	706 CATTTTGTGAGAGAGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGTTGAGAAAT 765
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QY	361 GTCTCTGCTTGGACTATCTACATTTCCGGAAAGATTGTACCGTGATCTCAAGTTGGAG 420
DB	
QY	766 GTCTCTGCTTGGACTATCTACATTTCCGGAAAGATTGTACCGTGATCTCAAGTTGGAG 825
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QY	421 AATCTAATGCTCGACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480
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QY	826 AATCTAATGCTCGACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 885
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QY	481 GGGATCACAGATGCGACCAACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACA 540
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QY	886 GGGATCACAGATGCGACCAACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACA 945
DB	
QY	541 GAGGTGTTAGAGATAAATGACTATGCGCGAGCAGTAGCTGTGGGGCCTAGGGGTTGTC 600
DB	
QY	946 GAGGTGTTAGAGATAAATGACTATGCGCGAGCAGTAGCTGTGGGGCCTAGGGGTTGTC 1005
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QY	601 ATGTATGAAATGATGTGGGAGGTTTACCTTTCTACAACCCAGGACCATCAGAAACTTTTT 660
DB	
QY	1006 ATGTATGAAATGATGTGGGAGGTTTACCTTTCTACAACCCAGGACCATCAGAAACTTTTT 1065
DB	
QY	661 GAATTAATTAATGGAAGACATTAATTTCTCGAACAATCTCTCTTCAGATGCAAAATCA 720
DB	
QY	1066 GAATTAATTAATGGAAGACATTAATTTCTCGAACAATCTCTCTTCAGATGCAAAATCA 1125
DB	
QY	721 TTGCTTTGAGGCTCTTGATTAAGGATCCAAATAAAGCGCTTGTGGAGGACCATGATGAT 780
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QY	1126 TTGCTTTGAGGCTCTTGATTAAGGATCCAAATAAAGCGCTTGTGGAGGACCATGATGAT 1185
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DB	
QY	1246 AAAAAAGCTTGACCTCTCTTTTAAAGCTCAAGTAAACATCTGAGACAGATACTAGATATTT 1305
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QY	901 GATGAAGAATTTACAGCTCAGACTATTAACAATAACACACCTGAAATAATATGATGAGAT 960
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QY	1306 GATGAAGAATTTACAGCTCAGACTATTAACAATAACACACCTGAAATAATATGATGAGAT 1365
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QY	961 GGTATGAGCTGCATGGAC 978
DB	
QY	1366 GGTATGAGCTGCATGGAC 1383
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RESULT 7	
BC020479	
LOCUS	BC020479
DEFINITION	Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma), mRNA (cdna clone IMAGE:3867931), partial cds.
ACCESSION	BC020479
VERSION	BC020479.1
KEYWORDS	GI:18042842
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 1445)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uscin, T.B., Toshnyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullhy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A.C., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1445)

NIH MGC Project
Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegue, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 13 Row: h Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 32307164.

FEATURES
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ORIGIN

Query Match	100.0%	Score 978	DB 8	Length 1445
Best Local Similarity	100.0%	Pred. No. 4.1e-206		
Matches 978	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	TCTACACCCATCATATAAAGACACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT	60	
Db	452	TCTACACCCATCATATAAAGACACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT	511	
Qy	61	AAAGGCACTTTTGGGAAGTTATTTTGGTTCGAGAGAAGCAAGTGGAAATATCTATGCT	120	
Db	512	AAAGGCACTTTTGGGAAGTTATTTTGGTTCGAGAGAAGCAAGTGGAAATATCTATGCT	571	
Qy	121	ATGAAGATTCTGAAGAAAGAGTCAATATTATGCAAAAGGATGAAGTGGCACACACTCTAACT	180	
Db	572	ATGAAGATTCTGAAGAAAGAGTCAATATTATGCAAAAGGATGAAGTGGCACACACTCTAACT	631	
Qy	181	GAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCTTGAATATTTCTTTC	240	
Db	632	GAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCTTGAATATTTCTTTC	691	
Qy	241	CAGACAAAACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	300	
Db	692	CAGACAAAACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	751	
Qy	301	CATTGTGCGAGAGCGGGTGTCTCTCTGAGGACCGCACACAGTCTTCTATGGTGCAAAATT	360	
Db	752	CATTGTGCGAGAGCGGGTGTCTCTCTGAGGACCGCACACAGTCTTCTATGGTGCAAAATT	811	
Qy	361	GTCTCTGCTTGGACATATCTACATTCGCGAAAGATTTGTGTACCGTGATCTCAAGTTGGAG	420	
Db	812	GTCTCTGCTTGGACATATCTACATTCGCGAAAGATTTGTGTACCGTGATCTCAAGTTGGAG	871	
Qy	421	AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGACATTTGCAAGAA	480	
Db	872	AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGACATTTGCAAGAA	931	
Qy	481	GGGATCACAGATGCAGCACCATCATGAAGACATTTCTGTGGCACCTCCAGAAATATCTGGCACA	540	
Db	932	GGGATCACAGATGCAGCACCATCATGAAGACATTTCTGTGGCACCTCCAGAAATATCTGGCACA	991	
Qy	541	GAGTGTGAAGAATAATGACTATGGCGGAGCAGTAGACTGGTGGGGCCCTAGGGGTTGTC	600	
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Qy	601	ATGTATGAATGATGTGTGGAGCTTACCTTTCTACAAACGAGGACCATGAGAACTTTT	660	
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Qy	721	TTGCTTTTCAGGGCTCTTGATTAAGGATCCAAATAAACGCCCTTGGTGAGGACCATGAT	780	
Db	1172	TTGCTTTTCAGGGCTCTTGATTAAGGATCCAAATAAACGCCCTTGGTGAGGACCATGAT	1231	
Qy	781	GCAAAAGAAATATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT	840	
Db	1232	GCAAAAGAAATATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT	1291	
Qy	841	AAAAAGCTTGCTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT	900	
Db	1292	AAAAAGCTTGCTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT	1351	
Qy	901	GATGAAGATTTACAGCTCAGATATTTACAAATAACACCACTGAAATAATGATGAGAT	960	
Db	1352	GATGAAGATTTACAGCTCAGATATTTACAAATAACACCACTGAAATAATGATGAGAT	1411	
Qy	961	GGTATGACATGCATGGAC	978	
Db	1412	GGTATGACATGCATGGAC	1429	

RESULT 8	Db	776	GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	835
BD251226	Qy	421	AATCTAATGCTGGACAAAGATGGCCACATAAAATAACAGATTTTGGACTTTGCAAAAGAA	480
LOCUS	Db	836	AATCTAATGCTGGACAAAGATGGCCACATAAAATAACAGATTTTGGACTTTGCAAAAGAA	895
DEFINITION	Qy	481	GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGGACCTCCAGACATATCTGGCACC	540
ACCESSION	Db	896	GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGGACCTCCAGACATATCTGGCACC	955
VERSION	Qy	541	GAGGTGTTTAGAAGATAATGACTATATGGCGAGCAGTAGACTTGTGGGGCTTAGGGGTTGTC	600
KEYWORDS	Db	956	GAGGTGTTTAGAAGATAATGACTATATGGCGAGCAGTAGACTTGTGGGGCTTAGGGGTTGTC	1015
SOURCE	Qy	601	ATGTATGAAATGANGTGTGGGAGGTACCTTTCTACAAACAGGACCATGAGAAACTTTTTT	660
ORGANISM	Db	1016	ATGTATGAAATGANGTGTGGGAGGTACCTTTCTACAAACAGGACCATGAGAAACTTTTTT	1075
	Qy	661	GAAATTAATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA	720
	Db	1076	GAAATTAATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA	1135
	Qy	721	TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAACCGCTTTGGTGGAGGACAGATGAT	780
	Db	1136	TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAACCGCTTTGGTGGAGGACAGATGAT	1195
	Qy	781	GCAAAAGAAATTTATGAGACACAGATTTCTTCTGAGTAAACTGGCAAGATGTATATGAT	840
	Db	1196	GCAAAAGAAATTTATGAGACACAGATTTCTTCTGAGTAAACTGGCAAGATGTATATGAT	1255
	Qy	841	AAAAAGCTTGACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATATTTT	900
	Db	1256	AAAAAGCTTGACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATATTTT	1315
	Qy	901	GATGAAGAATTTTACAGCTCAGACTATTACAAATAACCAACCTGAAATAATGATGAGGAT	960
	Db	1316	GATGAAGAATTTTACAGCTCAGACTATTACAAATAACCAACCTGAAATAATGATGAGGAT	1375
	Qy	961	GGTATGGAAGTGCATGGAC	978
	Db	1376	GGTATGGAAGTGCATGGAC	1393
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AR593589	LOCUS	AR593589	Sequence 1 from patent US 6809194.	
DEFINITION			Sequence 1 from patent US 6809194.	
ACCESSION		AR593589		
VERSION		AR593589.1	GI:56642796	
KEYWORDS			Unknown.	
SOURCE			Unknown.	
ORGANISM			Unclassified.	
REFERENCE			1 (bases 1 to 1547)	
AUTHORS			Reinhard, C. and Jefferson, A.B.	
TITLE			Akt3 inhibitors	
JOURNAL			Patent: US 6809194-A 1 26-OCT-2004;	
			Chiron Corporation; Emeryville, CA	
FEATURES			Location/Qualifiers	
	source		1..1547	
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ORIGIN				
Query Match			100.0%; Score 978; DB 6; Length 1547;	
Best Local Similarity			100.0%; Pred. No. 4.1e-206;	
Matches	978;	Conservative	0; Mismatches	0; Indels
				0; Gaps
				0;
Qy	1	TCTACAACCCATCATAAAGAAAGCAATGAATGATTTTGGACTATTTGAAACTACTAGGT	60	
Db	416	TCTACAACCCATCATAAAGAAAGCAATGAATGATTTTGGACTATTTGAAACTACTAGGT	475	
Qy	61	AAAGGCACATTTGGGAAAGTATTTTGGTTTCGAGAGAGGCAAGTGGAAAACTACTATGCT	120	
Db	476	AAAGGCACATTTGGGAAAGTATTTTGGTTTCGAGAGAGGCAAGTGGAAAACTACTATGCT	535	
Qy	121	ATGAAGATCTGAAGAAAGAGTCATTATTCGAAAGGATGAAGTGGCAGACACTCTAACT	180	
Db	536	ATGAAGATCTGAAGAAAGAGTCATTATTCGAAAGGATGAAGTGGCAGACACTCTAACT	595	
Qy	181	GAAAGCAGAGTATTAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATTCCTTC	240	
Db	596	GAAAGCAGAGTATTAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATTCCTTC	655	
Qy	241	CAGACAAAAGACCGTTTGTGTTTGGTGGTGAATATGTTAATGGGGCGAGCTGTTTTTC	300	
Db	656	CAGACAAAAGACCGTTTGTGTTTGGTGGTGAATATGTTAATGGGGCGAGCTGTTTTTC	715	
Qy	301	CAFTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCAGACAGTTCATGCTGAGAAAT	360	
Db	716	CAFTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCAGACAGTTCATGCTGAGAAAT	775	
Qy	361	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAG	420	

Dn	476	AAAGGCACCTTTTGGGAAAGTTATTTTGGTTTCGAGAGGCGAAGTGGAAAACTACTATGCT	535
Qy	121	ATGAAGATTCTGAAGAAAGAGTCAATTATTCGAAGGATGAAGTGGCACACACTCTAACT	180
Dn	536	ATGAAGATTCTGAAGAAAGAGTCAATTATTCGAAGGATGAAGTGGCACACACTCTAACT	595
Qy	181	GAAGACGAGATTAATAAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC	240
Dn	596	GAAGACGAGATTAATAAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC	655
Qy	241	CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC	300
Dn	656	CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC	715
Qy	301	CATTGTGCGAGAGCGGCTCTCTCGAGGACCGCACACGCTTCTATGTTGCGAAGATT	360
Dn	716	CATTGTGCGAGAGCGGCTCTCTCGAGGACCGCACACGCTTCTATGTTGCGAAGATT	775
Qy	361	GTCTCTGCTTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	420
Dn	776	GTCTCTGCTTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	835
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Qy	481	GGGATCACAGATGACGACCAATGAAGACATCTGTGGCACTCCAGAAATATCTGGCACCA	540
Dn	896	GGGATCACAGATGACGACCAATGAAGACATCTGTGGCACTCCAGAAATATCTGGCACCA	955
Qy	541	GAGGTGTTAGAGATTAATGATCTATGCGCGAGCAGTAGACTGGTGGGGCGAGCTGTTTTTC	600
Dn	956	GAGGTGTTAGAGATTAATGATCTATGCGCGAGCAGTAGACTGGTGGGGCGAGCTGTTTTTC	1015
Qy	601	ATGTATGAAATGATGTGGAGGTTACCTTTCTACAAACCGAGGACCATGAGAAACTTTTTT	660
Dn	1016	ATGTATGAAATGATGTGGAGGTTACCTTTCTACAAACCGAGGACCATGAGAAACTTTTTT	1075
Qy	661	GAATTAATTAATGAGAGACATTAATTTCTCGAAGACATCTCTTCAGATGCAAAATCA	720
Dn	1076	GAATTAATTAATGAGAGACATTAATTTCTCGAAGACATCTCTTCAGATGCAAAATCA	1135
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Dn	1136	TTGCTTTTCAGGGCTCTTGATAAAGAGTCCAAATAAAGCCCTTGGTGAGGACCAAGATGAT	1195
Qy	781	GCAAAAGAAATTAATGAGACACAGTTTTCTCTCGAGGTAAACTGGCAAGATGTATATGAT	840
Dn	1196	GCAAAAGAAATTAATGAGACACAGTTTTCTCTCGAGGTAAACTGGCAAGATGTATATGAT	1255
Qy	841	AAAAGCTTGTAACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT	900
Dn	1256	AAAAGCTTGTAACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT	1315
Qy	901	GATGAAGAAATTAACAGCTCAGACTATTAACAATAACACCACTGAAATAATGATGAGGAT	960
Dn	1316	GATGAAGAAATTAACAGCTCAGACTATTAACAATAACCACTGAAATAATGATGAGGAT	1375
Qy	961	GGTATGGACTGCATGGAC	978
Dn	1376	GGTATGGACTGCATGGAC	1393

RESULT 10
AX026529
LOCUS AX026529 1547 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 1 from Patent WO0037613.
ACCESSION AX026529
VERSION AX026529.1 GI:10187717
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.									
REFERENCE	1								
AUTHORS		Measure, S.L. and Richardson, A.							
TITLE		Human akt-3							
JOURNAL		Patent: WO 0037613-A 1 29-JUN-2000;							
		MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN PHARMACEUTICA NV (BE)							
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		Query Match	100.0.0%;	Score 978;	DB 6;	Length 1547;			
		Best Local Similarity	100.0.0%;	Pred. No. 4.1e-206;					
		Matches 978;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
Qy	1	TCTACAAACCCATATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT	60						
Dn	416	TCTACAAACCCATATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT	475						
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Dn	476	AAAGGCCACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT	535						
Qy	121	ATGAGATTTCTGAAGAAAGAGTCATTTTGCAGAGATGAAGTGGGCACACACTCTAACT	180						
Dn	536	ATGAGATTTCTGAAGAAAGAGTCATTTTGCAGAGATGAAGTGGGCACACACTCTAACT	595						
Qy	181	GAAGACGAGATTAATAAGAAACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC	240						
Dn	596	GAAGACGAGATTAATAAGAAACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC	655						
Qy	241	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	300						
Dn	656	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	715						
Qy	301	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAGAAATT	360						
Dn	716	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAGAAATT	775						
Qy	361	GTCTCTGCCCTTGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGCGAG	420						
Dn	776	GTCTCTGCCCTTGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGCGAG	835						
Qy	421	AATCTAATGCTGGACAAAGA TGGCCACATATAAATTA CAGATTTTGGACTTTTGCAAGAA	480						
Dn	836	AATCTAATGCTGGACAAAGA TGGCCACATATAAATTA CAGATTTTGGACTTTTGCAAGAA	895						
Qy	481	GGGATCACAGATGCGACCATGAAGACATCTGTGGGCACTCCAGAAATATCTGGGCACCA	540						
Dn	896	GGGATCACAGATGCGACCATGAAGACATCTGTGGGCACTCCAGAAATATCTGGGCACCA	955						
Qy	541	GAGGTGTTAGAAGATTAATGATCTATGGCCGAGCAGTAGACTGGTGGGGCGCTAGGGGTTGTC	600						
Dn	956	GAGGTGTTAGAAGATTAATGATCTATGGCCGAGCAGTAGACTGGTGGGGCGCTAGGGGTTGTC	1015						
Qy	601	ATGTATGAAATGATGTGGGAGGTTACCTTTCTACAAACCGAGGACCATGAGAAACTTTTTT	660						
Dn	1016	ATGTATGAAATGATGTGGGAGGTTACCTTTCTACAAACCGAGGACCATGAGAAACTTTTTT	1075						
Qy	661	GAATTAATTAATGGAAGACATTAATTTCTCGAAGACATCTCTTCAGATGCAAAATCA	720						
Dn	1076	GAATTAATTAATGGAAGACATTAATTTCTCGAAGACATCTCTTCAGATGCAAAATCA	1135						
Qy	721	TTGCTTTTCAGGGCTCTTGATAAAGAGTCCAAATAAAGCCCTTGGTGAGGACCAAGATGAT	780						
Dn	1136	TTGCTTTTCAGGGCTCTTGATAAAGAGTCCAAATAAAGCCCTTGGTGAGGACCAAGATGAT	1195						
Qy	781	GCAAAAGAAATTAATGAGACACAGTTTTCTCTCGGAGTAAACTGGCAAGATGTATATGAT	840						

Db	1196	GC	AAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT	1255
Qy	841	AAAAAGCTTGACCTCCCTTTAAACCTCAAGTAACATCTGAGACAGACTAGATATTTT	900	
Db	1256	AAAAAGCTTGACCTCCCTTTAAACCTCAAGTAACATCTGAGACAGACTAGATATTTT	1315	
Qy	901	GATGAAGATTTTACAGCTCAGACTATTACATATACACCACTGAAATAATGATGAGAT	960	
Db	1316	GATGAAGATTTTACAGCTCAGACTATTACATATACACCACTGAAATAATGATGAGAT	1375	
Qy	961	GGTATGGACTGCATGGAC	978	
Db	1376	GGTATGGACTGCATGGAC	1393	
RESULT 11				
LOCUS	HSA245709	1547 bp	mRNA	linear PRI 15-APR-2005
DEFINITION	Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).			
ACCESSION	AJ245709			
VERSION	AJ245709.1 GI:5804885			
KEYWORDS	Akt-3; Akt3 gene.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1			
AUTHORS	Masure,S., Haefner,B., Wesselink,J.J., Hoefnagel,E., Mortier,E., Verhassel,P., Tuytelaars,A., Gordon,R. and Richardson,A.			
TITLE	Molecular cloning, expression and characterization of the human serine/threonine kinase Akt-3			
JOURNAL	Eur. J. Biochem. 265 (1), 353-360 (1999)			
PUBMED	10491192			
REFERENCE	2 (bases 1 to 1547)			
AUTHORS	Masure,S.L.			
TITLE	Direct Submission			
JOURNAL	Submitted (25-AUG-1999) Masure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation, Turnhoutseweg 30, B-2340 Beerse, BELGIUM			
COMMENT	Phosphorylation at Thr305 and at Ser472 necessary for activation.			
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	KVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKQNRHPFLTSLKYSQTK			

3' UTR	DRLCFMVEYNGSELPHLSRERVFSEDRFRFYGAETIVSALDYLHSGKIVYRDLKLEI LMLDXXCHIKPTDFGLCKEGITDAAATWKTFCGTPEYLAPEVLNEDYIGRAVDWGLG VMYEMCGRIPLFQNDHEKLEFLLIMEDIKFPRTLSDDAKSLUSGLLIIDKPNKRLGGE PDDAKIMRHSFPFGWNQDYDKGLVPFPKQVTSSETDTRFYDEFTAQITITITPPE KYDDGDMDCMDNERRPHFPQFSYASGRE" 1451..>1547 /gene="Akt3"
ORIGIN	
Query Match	100.0%; Score 978; DB 8; Length 1547;
Best Local Similarity	100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 TCTACAAACCCATCATAAAGAAAGACAAATGAATGATTTTTCGAGAGAAAGCAAGTGGAAAAATACTATGCT 60
Db	416 TCTACAAACCCATCATAAAGAAAGACAAATGAATGATTTTTCGAGAGAAAGCAAGTGGAAAAATACTATGCT 475
Qy	61 AAAGGCACCTTTTGGGAAAGTATTATTTTGGTTTCGAGAGAAAGCAAGTGGAAAAATACTATGCT 120
Db	476 AAAGGCACCTTTTGGGAAAGTATTATTTTGGTTTCGAGAGAAAGCAAGTGGAAAAATACTATGCT 535
Qy	121 ATGAAGATTTCTGAAGAAAGAGTCAATTTATTCGAAAGGATGAAGTGGCACACACTCTAACT 180
Db	536 ATGAAGATTTCTGAAGAAAGAGTCAATTTATTCGAAAGGATGAAGTGGCACACACTCTAACT 595
Qy	181 GAAAGCAGATTTTAAAGAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTTCTTTC 240
Db	596 GAAAGCAGATTTTAAAGAACACATAGACATCCCTTTTAAACATCCTTTTAAACATCCTTTCTTTC 655
Qy	241 CAGACAAAGACCCGTTTGTCTTGTGATGATGATATGTTAATGGGGCGAGCTGTTTTTC 300
Db	656 CAGACAAAGACCCGTTTGTCTTGTGATGATGATATGTTAATGGGGCGAGCTGTTTTTC 715
Qy	301 CATTTGTCGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTCATGCTGTCAGAGAAAT 360
Db	716 CATTTGTCGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTCATGCTGTCAGAGAAAT 775
Qy	361 GTCTCTGCTTGGACTATCTACATTCGGAAGAGTGTGTACCGTGAATCTCAAGTTGCGAG 420
Db	776 GTCTCTGCTTGGACTATCTACATTCGGAAGAGTGTGTACCGTGAATCTCAAGTTGCGAG 835
Qy	421 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGACACTTTGCAAGAA 480
Db	836 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGACACTTTGCAAGAA 895
Qy	481 GGGATCACAGATGCAGCCACCATCAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db	896 GGGATCACAGATGCAGCCACCATCAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 955
Qy	541 GAGGTGTTTGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCCTAGGGGTTGTC 600
Db	956 GAGGTGTTTGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGGCCCTAGGGGTTGTC 1015
Qy	601 ATGTATGAAATGATGTGGGAGGTACTCTTTCTACACCAGGACCATGAGAACTTTTT 660
Db	1016 ATGTATGAAATGATGTGGGAGGTACTCTTTCTACACCAGGACCATGAGAACTTTTT 1075
Qy	661 GAAATTAATTAATGGAAGACATTAATAATTTCTCTCGAACACTCTCTTCAGATGCAAAATCA 720
Db	1076 GAAATTAATTAATGGAAGACATTAATAATTTCTCTCGAACACTCTCTTCAGATGCAAAATCA 1135
Qy	721 TTGCTTTTCAGGGCTCTTGTATAAGAGATCCAAATAAAGCCCTTGGTGGAGGACACAGATGAT 780
Db	1136 TTGCTTTTCAGGGCTCTTGTATAAGAGATCCAAATAAAGCCCTTGGTGGAGGACACAGATGAT 1195
Qy	781 GCAAAAGAAATTTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840
Db	1196 GCAAAAGAAATTTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1255
Qy	841 AAAAGAGCTTGTACCTCCTTTTAAACCTCAAGTACATCTGAGACAGACTAGATATTTT 900
Db	1256 AAAAGAGCTTGTACCTCCTTTTAAACCTCAAGTACATCTGAGACAGACTAGATATTTT 1315

3' UTR	DRLCEVMYVNGBELFPHLSRVPSEDRTRFYGAIEVSALDYLSHGKIVYRDLKLEN LMLDKDGHKILDTGLCKEIGTDAATMTKTCFETPEYLAPEVLEDNDYGRAVDMWGLGV VNYEMCCRLFPFYQDHEKLFELIMEDIKFPRTLSSDAKSLLSLLIKOPNRKLGCG PDDAKEINRHSFFGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEEFTAQITITPPE KYDEGMDCMONERRPPFPQSASGRE" 1451..>1547 /gene="Akt3"			
ORIGIN	Query Match 100.0%; Score 978; DB 8; Length 1547; Best Local Similarity 100.0%; Pred. No. 4.1e-206; Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	TCTACAA	CCCATCATAAAGAAAGACAATGAATGATGATTTTGTGACTATTGAACTACTAGGT	60
Db	416	TCTACAA	CCCATCATAAAGAAAGACAATGAATGATGATTTTGTGACTATTGAACTACTAGGT	475
Qy	61	AAAGGCAC	CTTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAAACTACTATGCT	120
Db	476	AAAGGCAC	CTTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAAACTACTATGCT	535
Qy	121	ATGAAGAT	TTCTGAAGAAAGAAAGTCAATTTATGCAAAAGGATGAAGTGGCACACACTCTAACT	180
Db	536	ATGAAGAT	TTCTGAAGAAAGAAAGTCAATTTATGCAAAAGGATGAAGTGGCACACACTCTAACT	595
Qy	181	GAAAGCAG	ATTTAAAGAACACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTTC	240
Db	596	GAAAGCAG	ATTTAAAGAACACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTTC	655
Qy	241	CAGACAAA	AGACCGTTTCTGTTGTTGATGGATATGTTTAAATGGGGGCGAGCTGTTTTC	300
Db	656	CAGACAAA	AGACCGTTTCTGTTGTTGATGGATATGTTTAAATGGGGGCGAGCTGTTTTC	715
Qy	301	CATTTGTG	AGAGAGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAAAT	360
Db	716	CATTTGTG	AGAGAGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAAAT	775
Qy	361	GTCTCTGC	CTTGGACTATCTACATTCGGAAGATGTTGTACCGTATCTCAAGTTGGAG	420
Db	776	GTCTCTGC	CTTGGACTATCTACATTCGGAAGATGTTGTACCGTATCTCAAGTTGGAG	835
Qy	421	AATCTAAT	GCTGGACAAAGATGGCCACATAAATAATACAGATTTTGGACTTTGCAAGAA	480
Db	836	AATCTAAT	GCTGGACAAAGATGGCCACATAAATAATACAGATTTTGGACTTTGCAAGAA	895
Qy	481	GGGATCAC	AGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGCACCA	540
Db	896	GGGATCAC	AGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGCACCA	955
Qy	541	GAGGTGTT	AGAAAGATAATGACTATGCGCGAGCAGTAGACTGTGTGGGGCCTAGGGGTTGTC	600
Db	956	GAGGTGTT	AGAAAGATAATGACTATGCGCGAGCAGTAGACTGTGTGGGGCCTAGGGGTTGTC	1015
Qy	601	ATGATATA	GAATGATGTTGGGAGGTACCTTTCTACAAACGAGGACCATGAGAACTTTT	660
Db	1016	ATGATATA	GAATGATGTTGGGAGGTACCTTTCTACAAACGAGGACCATGAGAACTTTT	1075
Qy	661	GAATTAAT	TAATGGAAGACATTAATAATTTCTCGAAACACTCTCTTCAGATGCAAAATCA	720
Db	1076	GAATTAAT	TAATGGAAGACATTAATAATTTCTCGAAACACTCTCTTCAGATGCAAAATCA	1135
Qy	721	TTGCTTTT	CAGGGCTCTTGTATAAAGGATCCAAATAAAACGGCTTGGTGAGGACCAAGATGAT	780
Db	1136	TTGCTTTT	CAGGGCTCTTGTATAAAGGATCCAAATAAAACGGCTTGGTGAGGACCAAGATGAT	1195
Qy	781	GCAAAAGA	AATATATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGATATGAT	840
Db	1196	GCAAAAGA	AATATATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGATATGAT	1255
Qy	841	AAAAAGCT	TGTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGACTAGATATTTT	900
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Db 1376 GGTATGGAATGCATGGAC 1393
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CQ714620
LOCUS CQ714620 1651 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 554 from Patent WO02068579.
ACCESSION CQ714620
VERSION CQ714620.1 GI:42275477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 554 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1..1651
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 978; DB 6; Length 1651;
Best Local Similarity 100.0%; Pred. No. 4e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCTACACCCATCATAAAGAAGACAAATGAATGATTGTGACTATTGAAACTACTAGGT 60
Db 361 TCTACACCCATCATAAAGAAGACAAATGAATGATTGTGACTATTGAAACTACTAGGT 420
Qy 61 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATACATGCT 120
Db 421 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATACATGCT 480
Qy 121 ATGAAGATTCTGAAGAAAGAGTCATTATTGCAAGAGGATGAAGTGGCACACACTCTAACT 180
Db 481 ATGAAGATTCTGAAGAAAGAGTCATTATTGCAAGAGGATGAAGTGGCACACACTCTAACT 540
Qy 181 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCTTGAATAATTCCTTC 240
Db 541 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCTTGAATAATTCCTTC 600
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTATGGGGGAGCTGTTTTC 300
Db 601 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTATGGGGGAGCTGTTTTC 660
Qy 301 CATTTGTCGAGAGCGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAAGAAATT 360
Db 661 CATTTGTCGAGAGCGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAAGAAATT 720
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAGAAGTTGTTACCGTGATCTCAAGTTGGAG 420
Db 721 GTCTCTGCTTGGACTATCTACATTCGGAAGAAGTTGTTACCGTGATCTCAAGTTGGAG 780
Qy 421 AATCTAATGCTGGCAAGATGGCCACATAAAATTACAGATTTTGGACTTTGCAAGAA 480
Db 781 AATCTAATGCTGGCAAGATGGCCACATAAAATTACAGATTTTGGACTTTGCAAGAA 840
Qy 481 GGGATCACAGATGCAGGCCACCATGAAGACATTCTGTGGCACTCCAGAAATATCTGGCACCA 540

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Db 1321 GGTATGACTGCATGGAC 1338
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AF085234
LOCUS AF085234 1706 bp mRNA linear PRI 12-DEC-2001
DEFINITION Homo sapiens STK-2 mRNA, complete cds.
ACCESSION AF085234
VERSION AF085234.1 GI:17529662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1706)
AUTHORS Li,X., Yu,L., Huang,H., Zhang,M., Zhao,Y. and Zhao,S.
TITLE Cloning of a novel human cDNA, STK-2, which encodes a rat
serine-threonine protein kinase (STK) homolog
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1706)
AUTHORS Zhao,Y.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-1998) Zhao Y., Institute of Genetics, Fudan
University, Lab of Human Gene Research, No. 220, Handan Road,
Shanghai, People's Republic of China, 200433
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
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ORIGIN

Query Match 100.0%; Score 978; DB 8; Length 1706;
 Best Local Similarity 100.0%; Pred. No. 4e-206;
 Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCTACACCCATCATAAAGAAAGACAAATGAATGATTTTGACATATTTGAAACTACTAGGT	60
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QY	61	AAAGGCACCTTTTGGGAAAGTTATTTCGTTTCGAGAGAGGCAAGTGGAAATACTATGCT	120
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QY	121	ATGAAGATTCTGAAGAAGAGTCAATTTATGCAAAAGGATGAAGTGGCACACCTCTAACT	180
DB	573	ATGAAGATTCTGAAGAAGAGTCAATTTATGCAAAAGGATGAAGTGGCACACCTCTAACT	632
QY	181	GAAGCAGAGTATTAAAGACACATAGACATCCCTTTTAACTCCCTTGAATAATTCCTTC	240
DB	633	GAAGCAGAGTATTAAAGACACATAGACATCCCTTTTAACTCCCTTGAATAATTCCTTC	692
QY	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC	300
DB	693	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC	752
QY	301	CATTTGTGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTTCTATGTTGAGAAAT	360
DB	753	CATTTGTGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTTCTATGTTGAGAAAT	812
QY	361	GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	420
DB	813	GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	872
QY	421	AATCTAATGCTGGCAAAAGATGGCCACATAAAATTAACAGATTTTGACATTTGCAAGAA	480
DB	873	AATCTAATGCTGGCAAAAGATGGCCACATAAAATTAACAGATTTTGACATTTGCAAGAA	932
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DB	933	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	992
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DB	993	GAGGTGTTAGAGATAATGACTATGGCCGACGATAGACTGTTGGGCGCTTAGGGTTGTC	1052
QY	601	ATGTPATCAATGATGTGGGAGTTACCTTTCTACAAACGAGCCCATGAGAACTTTTT	660
DB	1053	ATGTPATCAATGATGTGGGAGTTACCTTTCTACAAACGAGCCCATGAGAACTTTTT	1112
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DB	1113	GAATTAATAATTAATGGAAGACATTAATTTCCCTCGAACATCTCTTCAGATGCAAAATCA	1172
QY	721	TTCGTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCGCTTGGTGGAGGACGAGATGAT	780
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QY	781	GCAAAAGAAATATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT	840
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BD260777
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Human protein kinase B-gamma polypeptide and method of degrading
nonhuman protein kinase B-gamma.
ACCESSION BD260777
VERSION BD260777.1 GI:33070547
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Hominidae; Homo.
1 (bases 1 to 2367)
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AUTHORS Attersand, A.
TITLE Human protein kinase B-gamma polypeptide and method of degrading
nonhuman protein kinase B-gamma
JOURNAL Patent: JP 2002539823-A 1 26-NOV-2002;
BIOVITRUM AB
COMMENT OS Homo sapiens (human)
PN JP 2002539823-A/1

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PF 23-MAR-2000 JP 2000608727
PR 25-MAR-1999 SE 9901115-7
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PC C12N15/09,A01K67/027,C07K16/40,C12N1/15,C12N1/19,C12N1/21,PC
C12N5/10,
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